OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.7
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Run on:     March  3, 2006, 15:25:40 ; Search time 316 Seconds
                                       (without alignments)
                                       3617.000 Million cell updates/sec

Title:          US-10-736-868-2
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                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
                Delop    6.0 , Delext   7.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:     2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  Issued_Patents_NA:*
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    8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | 171 | 5.2 | 100990 | 3 | | US-09-409-800B-2 | Sequence 2, Appli |
| 2 | 169.5 | 5.2 | 6151 | 3 | | US-09-799-451-528 | Sequence 528, App |
| 3 | 162.5 | 4.9 | 5883 | 3 | | US-09-949-016-5001 | Sequence 5001, Ap |
| 4 | 159 | 4.8 | 2680 | 2 | | US-08-533-306A-5 | Sequence 5, Appli |
| 5 | 159 | 4.8 | 2680 | 2 | | US-08-742-923A-5 | Sequence 5, Appli |
| 6 | 159 | 4.8 | 2887 | 2 | | US-08-533-306A-3 | Sequence 3, Appli |
| 7 | 159 | 4.8 | 2887 | 2 | | US-08-742-923A-3 | Sequence 3, Appli |
| 8 | 159 | 4.8 | 4935 | 3 | | US-09-949-016-1019 | Sequence 1019, Ap |
| 9 | 159 | 4.8 | 4935 | 3 | | US-09-949-016-5054 | Sequence 5054, Ap |
| 10 | 159 | 4.8 | 5574 | 3 | | US-09-917-254-40 | Sequence 40, Appl |
| 11 | 159 | 4.8 | 6861 | 3 | | US-09-949-016-1240 | Sequence 1240, Ap |
| 12 | 159 | 4.8 | 6861 | 3 | | US-09-949-016-1241 | Sequence 1241, Ap |
| 13 | 159 | 4.8 | 6861 | 3 | | US-09-949-016-1242 | Sequence 1242, Ap |
| 14 | 158.5 | 4.8 | 19269 | 3 | c | US-09-902-540-1175 | Sequence 1175, Appl |
| 15 | 157 | 4.8 | 6175 | 3 | | US-08-875-435B-1 | Sequence 1, Appli |
| 16 | 157 | 4.8 | 6856 | 3 | | US-09-566-921-42 | Sequence 42, Appl |
| 17 | 156 | 4.7 | 3807 | 3 | | US-09-645-456A-8 | Sequence 8, Appli |
| 18 | 156 | 4.7 | 3807 | 3 | | US-09-425-324A-8 | Sequence 8, Appli |
| 19 | 156 | 4.7 | 3807 | 3 | | US-09-645-791-8 | Sequence 8, Appli |
| 20 | 155.5 | 4.7 | 3972 | 3 | | US-09-645-456A-6 | Sequence 6, Appli |
| 21 | 155.5 | 4.7 | 3972 | 3 | | US-09-425-324A-6 | Sequence 6, Appli |
| 22 | 155.5 | 4.7 | 3972 | 3 | | US-09-645-791-6 | Sequence 6, Appli |
| 23 | 153.5 | 4.7 | 6396 | 3 | | US-09-949-016-3344 | Sequence 3344, Ap |
| 24 | 153 | 4.6 | 9551 | 2 | | US-08-056-200-93 | Sequence 93, Appl |
| 25 | 153 | 4.6 | 9551 | 2 | c | US-08-800-644-93 | Sequence 93, Appl |
| 26 | 152.5 | 4.6 | 1761 | 3 | c | US-09-252-991A-16401 | Sequence 16401, A |
| 27 | 152.5 | 4.6 | 3489 | 3 | | US-09-252-991A-16193 | Sequence 16193, A |
| 28 | 152.5 | 4.6 | 4055 | 3 | | US-09-688-188B-10 | Sequence 10, Appl |
| 29 | 152.5 | 4.6 | 4055 | 3 | | US-09-291-417D-10 | Sequence 10, Appl |
| 30 | 152 | 4.6 | 3831 | 3 | | US-09-645-456A-5 | Sequence 5, Appli |
| 31 | 152 | 4.6 | 3831 | 3 | | US-09-425-324A-5 | Sequence 5, Appli |
| 32 | 152 | 4.6 | 3831 | 3 | | US-09-645-791-5 | Sequence 5, Appli |
| 33 | 151.5 | 4.6 | 3996 | 3 | | US-09-645-456A-2 | Sequence 2, Appli |
| 34 | 151.5 | 4.6 | 3996 | 3 | | US-09-425-324A-2 | Sequence 2, Appli |
| 35 | 151.5 | 4.6 | 3996 | 3 | | US-09-645-791-2 | Sequence 2, Appli |
| 36 | 151.5 | 4.6 | 6644 | 3 | | US-08-875-435B-5 | Sequence 5, Appli |
| 37 | 150.5 | 4.6 | 3228 | 3 | | US-09-252-991A-1816 | Sequence 1816, Ap |
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| 39 | 150.5 | 4.6 | 4209 | 3 | | US-09-248-796A-400 | Sequence 400, App |
| 40 | 150.5 | 4.6 | 7596 | 3 | | US-09-023-655-1463 | Sequence 1463, Ap |
| 41 | 149 | 4.5 | 2130 | 3 | | US-09-248-796A-4942 | Sequence 4942, Ap |
| 42 | 148.5 | 4.5 | 2094 | 3 | | US-09-248-796A-1868 | Sequence 1868, Ap |
| 43 | 146.5 | 4.5 | 3894 | 3 | | US-09-645-456A-7 | Sequence 7, Appli |
| 44 | 146.5 | 4.5 | 3894 | 3 | | US-09-425-324A-7 | Sequence 7, Appli |
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ALIGNMENTS

RESULT 1
US-09-409-800B-2
; Sequence 2, Application US/09409800B
; Patent No. 6706522
; GENERAL INFORMATION:
;  APPLICANT: Blattner, Frederick R.
;  APPLICANT: Burland, Valerie
;  APPLICANT: Rose, Debra J.
;  APPLICANT: Mayhew, George F.
;  APPLICANT: Perna, Nicole
;  APPLICANT: Perry, Robert D.
;  APPLICANT: Straley, Susan C.
;  APPLICANT: Fetherston, Jacqueline D.
;  APPLICANT: Lindler, Luther E.
;  APPLICANT: Plano, Gregory V.
;  TITLE OF INVENTION: Plasmid DNA From Yersinia Pestis
;  FILE REFERENCE: 960296.95939
;  CURRENT APPLICATION NUMBER: US/09/409,800B
;  CURRENT FILING DATE: 1999-09-30
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 2
;  LENGTH: 100990
;  TYPE: DNA
;  ORGANISM: Yersinia pestis
US-09-409-800B-2

Alignment Scores:
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Score:                    171.00          Matches:        142
Percent Similarity:       34.0%           Conservative:   100
Best Local Similarity:    19.9%           Mismatches:     260
Query Match:              5.2%            Indels:         210

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Qy    39  ------LysSerHisGlnLeuProLeuAlaProSerMetGluAlaLeuGluLeu  55
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Db 85345  ATGAAGATGCCGACGAGAAAAGGCTCCGTCCGATCACACTGACGGCGCAAGGAAAATGAGGATGCC  85401

Qy    56  MetGlyValGlnPheValAspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGly  75
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Db 85402  ------GACGTTTTATTGAACGGACAGAATGGGACAGGTATTCAACGGA  85443

Qy    76  AlaPheLysThrGlnLeuGluValLeuGluLysValHisProAspGlnPheAspLysTyr  95
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Db 86389  GAGGACGCACTCAAG--GCGCTCGACGAGATGGAAGAAGGAACAGACGAAATGACCGAA  86445

Qy   423  ProLysProGlnProGlyTyrPheAlaProAlaProIleProThrArgLysIleProThrArgLysMet  442
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Qy   443  LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArg----------  459
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Db 86530  ----------ATCGGGTTGATTGATGAGGCTGAAGAGCATGTAAAACGCACCAGAAAG  86577

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Db 86578  ACATTCGGCGCAATCCCAATGCACTCCACCTGTCGATCGCATGGTTCCGGAAGGC  86637

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Qy   543  ------ArgProIleProProLeuPheGluProLeuLysProGlyArg  555
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Qy   556  HisThrArgLeuArgTrpThrGlyArgAlaAsnGluLysProGlyLeuLysSerArg----------  575
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Qy   594  ThrGlnGlyArgAlaArgAspGluTrpAspGluThrMetPheLys  607
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RESULT 2
US-09-799-451-528
; Sequence 528, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Yamazaki, Victoria
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Reena
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6783969el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 803
;  CURRENT APPLICATION NUMBER: US/09/799,451
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 948
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 528
;   LENGTH: 6151
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (263)..(3133)
US-09-799-451-528

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Percent Similarity:      36.3%         Conservative:   108
Best Local Similarity:   18.9%         Mismatches:     248
Query Match:             5.2%          Indels:         149
DB:                      3             Gaps:           22

US-10-736-868-2 (1-643) x US-09-799-451-528 (1-6151)

Qy          36 LeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGluLeu 55
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Qy          56 MetGlyValGlnPheValAspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGly 75
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Db         689 AGAGACAGCACAATGTTAGATCTTCAGGCCCAGCTGAAAGAACTGCAGAGAGAGAATGAC 748

Qy          76 AlaPheLysThrGlnLeuGluValLeuGluLysValHisProAspGlnPheAspLysTyr 95
                     :::   :::|||::::::   :::                     :::
Db         749 CTCCTCCGGAAAGAGCTAGACATCAAGGACAGCAAATTGGGATCTTCCATGAACAGTATT 808

Qy          96 LysLysLeuLysValAspAspLeuAlaAlaAspAlaValMetGlnGlnAlaGluMetAla 115
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Db         809 AAGACTTTCTGGAGTCCTGAGCTTAAGAAGGAGAGAGTCTTGAGGAAAGAAGAGGCAGCG 868

Qy         116 LysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIlePro 135
               ::::::                        :::                     :::
Db         869 CGGATGTCTGTCCTCAAGGAGCAGATGAGGGTTTCCCATGAAGAAAATCAGCACCTACAG 928

Qy         136 IleGlySerSerIleArgGlyLeuGluAspAlaIleArgThrGlnArgAspMetGluAsn 155
               :::      :::|||:::   |||:::|||   :::|||||||||||||||:::   :::
Db         929 TTG------ACAATCCAGGCCCTTCAAGATGAGCTGCGAACCCAGAGAGACCTCAACCAC 982

Qy         156 ThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPheGlnThrGlnIleLeu 175
                           |||         :::         :::   |||      ::::::
Db         983 CTCCTCCAGCAAGAGAGTGGCAACCGAGGAGCG---GAGCACTTCACCATCGAGCTGACC 1039

Qy         176 ProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPheLysMetProGlnGlnMet 195
                                             :::      |||:::      |||
Db        1040 ------------------------------GAGGAGAACTTTAGGCGGCTCCAAGCCGAG 1069

Qy         196 ArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAlaLeuAlaGlnArgAlaMet 215
                        ||||||            :::   ::::::   |||   :::      :::
Db        1070 CATGACAGGCAGGCTAAGGAGCTGTTCCTTTTGAGGAAGACATTAGAGGAAATGGAGCTG 1129

Qy         216 LeuGlyLysAsnAlaProValAlaGlyGlyArgGlyGluGluGlnArgMetMetMetAsn 235
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Db        1130 ------------------------------AGAATTGAAACGCAGAAACAAACCCTCAAT 1159

Qy         236 ArgValAspGlnArgMetGlnGln------ArgGluLeuGlnGluGluAspGluAspAsp 253
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Db        1160 GCCCGAGATGAGTCAATTAAAAAACTTCTTGAGATGTTGCAAAGTAAAGGCTTGCCATCC 1219

Qy         254 AspAspLeuGluAspGluAspValProArgArgArgSerSerAspGlyGluProGln--- 272
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Db        1220 AAAAGCCTGGAGGATGACAATGAGCGAACGCGGCGGATGGCAGAGGCTGAGTCTCAGGTC 1279

Qy         273 ------------------------------------SerGluAlaGluHisGlnArgArgAsp 281
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Db        1280 AGCCACTTGGAAGTGATTTTAGATCAGAAAGAGAAGGAAAACATACATCTTAGAGAGGAA 1339

Qy         282 LeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGluVal 301
               |||   ||||||   :::      |||                  :::   |||:::
Db        1340 TTGCACCGAAGAAGCCAACTTCAGCCG------------------GAGCCAGCCAAGACG 1381

Qy         302 GlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu 321
               ::::::|||   :::         |||:::|||:::   ::::::            |||
Db        1382 AAGGCTCTCCAGACTGTCATCGAAATGAAGGACACAAAAATCGCTTCA---------TTG 1432

Qy         322 AlaMetAsnAspGluAsp---GluSerAlaPheArgAlaMetGluAlaArgAlaLysLeu 340
                     |||      |||   |||         :::   ::::::|||         |||
Db        1433 GAACGAAACATAAGGGATCTTGAGGATGAGATCCAGATGTTAAAAGCCAATGGTGTGCTG 1492

Qy         341 AspGlnLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGluSerAspAspAspGlu 360
                                                                  :::   |||
Db        1493 ---------------------------------------------------AACACTGAG 1501

Qy         361 AspGluGluAspGluAsnLeuIleAspProSerGluAsnSerPheArgArgAlaProLeu 380
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Db        1502 GACCGCGAAGAAGAG--------------------------------------------- 1516

Qy         381 ArgLeuSerSerGlyPheValGluLysLeuLysSerAsnAspGluLeuLysSerAlaLeu 400
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Db        1517 ---------------------------ATCAAACAAATTGAGGTTTACAAAAGTCACTCC 1549

Qy         401 AspArgIleLysTyrArgValAspAspValGluLysTyrLeuAlaProLysProMetGlu 420
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Db        1550 AAGTTTATGAAGACCAAGATTGATCAGCTGAAGCAGGAACTTTCAAAGAAAGAGTCGGAA 1609

Qy         421 PheAsnProLysProGlnProGlyTyrPheAlaProArgLysIleProThrArgProArg 440
                                                      |||:::   |||
Db        1610 CTT---------------------CTTGCCTTACAAACAAAGCTTGAAACCCTCAGCAAT 1648

Qy         441 LysMetLeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArgHis 460
               :::                     ||||||   |||         |||:::   :::
Db        1649 CAA------------------AATTCAGATTGCAAGCAACACATTGAAGTGCTCAAAGAG 1690

Qy         461 ProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn 480
                     |||            |||||||||   |||            |||:::
Db        1691 TCACTTACT------------GCCAAAGAACAGAGGGCTGCCATC---CTTCAGACTGAG 1735

Qy         481 ProSerLeuAlaAlaLeuPheMetAspAspLys---------LeuGluAsnThrLeuLys 497
                              |||   :::::::::|||         |||            |||
Db        1736 GTAGATGCGCTGAGATTACGACTGGAAGAAAAAGAATCTTTCCTCAATAAAAAAACAAAA 1795
```

Qy   498 GlyArgGlnMetLeuThrAspGluThrGlnLysGlyArgThrArgValLysThrIleArgAla 517
                                                                    |||||||||
Db  3920 AGTCCCAGCTGCAGGACACTCAGGAGCTG-CTGCAGGAGGAGAACCGGCAGAAGCTGAGC 3978

Db  1796 CAGCTTACAGGACCTCACA--GAAGAGAGGGG 1825
Qy    46 LeuAlaProSerMetGluAlaLeuGlu--  54
Db  3979 CTGAGCACCAAGCTCAGCAGCTGGAGGACGAAGAAGAATTCCTTCCGGAGCCAGCTGGAG 4038

Qy   518 LeuProArgLeuPheGlyAlaProThrAlaLysAlaGluMetIleAspAlaLysAlaLysValPhe 537
Db    55 --------------------LeuMetGlyValGlnPhe  60
Db  1826 --------------------ACACTGGCCGGTGAAATTCGTGACATGAAAGATATG 1861
Db  4039 GAGGAGGAGGAGGCCAAGCAACCTGGAGAGCAGATCGCCACCCTCCATGCCCAGGTG 4098

Qy   538 GlnAspIleGluGluArgProIleProProLeuPheGluProLysGlyArgHisThr 557
Qy    61 ValAspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGlyAlaPheLysThrGln  80
Db  1862 TTAGAGATGAAGCAGAAAGAAAAATCAATGTTCTTCAGAAAAGAATTGAAAACTTGCAAGAA 1921
Db  4099 GCCGAC--------ATGAAAAAGAGATGGAGGACCAGTGTGGGTGCCTGGAAACTGCT 4149

Qy   558 ArgLeuArgTrpThrGlyAlaAsnGluLysValSerGlyIleProGlyLeuGlySerArgPheIle 577
Qy    81 LeuGluValLeuGluLysValHisProAsp  90
Db  1922 CAACTTAGG-------GATAAAGACAACTGACCAACCTGAAAGACAGA-------- 1966
Db  4150 GAGGAGGTGAAGAAGAGCTTCCAGAAGACCACCTGGAGGGGCCTGAGCCAGCGGCGGCGAGGAG 4209

Qy   578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaSerThr------- 594
Qy    91 --------GlnPheAspLysTyrLysLysLys---         ValAsp 101
Db  1967 GTGAAGTCCTTGCAGACGGATTCCAGTAATACAGATACTGCACTGGCACGCTGAGGAA 2026
Db  4210 AAGGTGCCGCCTACGCAACAGCTGGAGAACCAAGACGCGGCCTGCAGCAGGAGCTGGAC 4269

Qy   595 GlnGlyArgAlaArgAspGlu 601
Qy   102 AspLeuAlaLeuAlaAspAlaValMetGlnGlnIleAlaAlaGluMetAlaLysLeuGlnProLysSer 121
Db  2027 GCTCTGTCAGGAGGAGGAGAATAATTGAGCGTTGAAGAACAGCCGAGAAAGATGAT 2086
Db  4270 GACCTGCTGGTGGACCTGGACCACCAGCTGCCAGAGCGCGTGCAACCTGGAGAAGAAGCAG 4329

Qy   602 TrpAspThrMetPheLysIleProAsnAsnTrpAsnProGlyAspGluValGlyPheLys 621
Qy   122 GlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIleProIleGly------ 137
Db  2087 CGGGAAAGACTAGAAGAGATAGAATCCTTCCGAAAAGAGAACAAAGACCTGAAAGAGAAG 2146
Db  4330 AAGAAG------TTTGACCCAGCTCCTGGCGGAGCAGAAGACCATCTCTGCCAAGTATGCA 4383

Qy   622 MetAsnSer 624
Qy   138                                                  SerSer 139
Db  2147 GTCAATGCT 2155
Db  4384 GAGGAGCGGCGACCGGCTGAGCGGGAGGCCCGAGAGAGGAGACCAAGGCTCTGTCGCTG 4443

Qy   140 IleArgGlyLeuAspAlaIleAlaArgThrArgGlnMetGluAsnThrArgAspMetProSer 159
Db  4444 GCCCGGGCCCTGGAGGAAGCCATGAGCGAGCAGGAGCAGGAGGCCGAGCTGGAGCGGCTCAAC--- 4497

Qy   160 GluGlnIleAlaAlaValMetAspLysPheGlnThrGlnIleLeuLeuProGlyLeuVal 179
Db  4498 -----------------AAGCAGTTCCGACGGAG-------ATG 4518

Qy   180 AlaAsnMetIleAlaGlyLysAsnProPhe-----LysMetProGlnGlnMetArgLysAla 198
Db  4519 GAGGACCTTATGAGCGTCCAAGCATGATGTGGGCAAGAGTGTCCAGGAGGCTGGAGAAGTC- 4577

Qy   199 GlnIleAlaAlaProSerValPheGlnGlnIleAlaLeuAlaLeuAlaGlnAlaMetLeuGlyLysLys 218
Db  4578 CAAGCGGCGGCCCT----------------------AGAGCAGCAGGTGGAGGA 4607

Qy   219 Asn-----AlaProValAlaGlyValGlyGluGlyGlnLysArgMetMetAsn 235
Db  4608 GATGAAGACGTGAAGAGGCTGGAAGGACGAGCTGCAGCGGACGAAGATGCCAAGCT 4667

Qy   236 -ArgValAspGlnArgMetGln 249
Db  4668 GCGGTTGGAGGTTCAACCTGCAGGCCATGAAGACGCCCAGTTCGAAGCGGCCG 4727

Qy   249 uAspGluAspAspAspAspLeuGluAspGluAspGlnSerProSerAspGl 269
Db  4728 GGACGAGCAGCGGGAGGAGAAGAAGAGCAGCTGGTTCAGAGGATGCGGGAGATGGAGGC 4787

Qy   269 yGluProGlnSerGluUlaHisGlnHisGlnAspArgAspArgLeuLysSerSe 289
Db  4788 AGAGCTGGAGGACAGCGAGAAGCAGCGCCTCGATGGAGCCGCCCGGAAGAAGCTGGA 4847

Qy   289 rProArgLeuLysGluLeu------- 295
Db  4848 GATGGAGACCTGAAGGACCTGGAGGCTCACGTCGACTCGGCAGCAAGAACCGGGACGAAGC 4907

Qy   296 --------LeuGlnAsnAlaGluValAlaGlnAlaLeuSerLeuSerGlnTyrGlnArgMetArgAs 312
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RESULT 3
US-09-949-016-5001
; Sequence 5001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5001
; LENGTH: 5883
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5001

Alignment Scores:
Pred. No.:              4.54e-06          Length:        5883
Score:                  162.50            Matches:       136
Percent Similarity:     35.9%             Conservative:  88
Best Local Similarity:  21.8%             Mismatches:    213
Query Match:            4.9%              Indels:        192
DB:                     3                 Gaps:          25

US-10-736-868-2 (1-643) x US-09-949-016-5001 (1-5883)

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Qy    12 GlyPheCysIleAlaProLeuSer-----AlaGlnSerProSerThrSerAsp------  27
Db  3860 GGCTTCTCAGCCAGTCCGACGCAGTCCAGCAAGCTCACCAAGGACTTCTCCGGCGCTGG 3919

Qy    28 AlaProGly-----AlaLeuLeuSerSerLeuValGlyLysSerHisGlnLysLeuPro  45
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```
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869COB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2680 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Sample 2
TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
TISSUE TYPE: subtype (inv16)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 16[inv(16) (p13q22)]
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2451
US-08-533-306A-5

Alignment Scores:
Pred. No.:               3.08e-06       Length:          2680
Score:                   159.00         Matches:          150
Percent Similarity:      38.3%          Conservative:     130
Best Local Similarity:   20.5%          Mismatches:       230
Query Match:             4.8%           Indels:           225
DB:                      2              Gaps:              35

US-10-736-868-2 (1-643) x US-08-533-306A-5 (1-2680)
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Db  4908  CATCAAACAGCTGCGGAAGCTGCAGGCCCAGATGAAGGACTGCATGCGCGAGCTGGATGA  4967
Qy  312   pSerProLeuSerLysArgArgProLeuAlaMetAsnAspGluArgGluSerAlaPheAr  332
                   ||:::        ||      |||:|||
Db  4968  CACCCGCGCCTCGTGAGGAGATCCTGGCCCAGGCCAAAGAGAGAACGAGAGAAGCTGAA  5027

Db  5028  GAGCATGGAGGCC----------GAGATGATCCAGTTGCAGGAGGAACTGCGAGC  5072
Qy  332   gAlaMetGlyAlaAlaArgAlaLysLeuAspLeuSerGlnLysSerGlnLeuValLeuHisGl  352
                   :::||||||
Qy  352   yPheGlyGluSerAspAspAspGluAspGluAspAspGluAsnLeuIleAspProSerGl  372
                   |||||   ::: |||    |||
Db  5073  CGCGGAGCGGTGCCAAGCGCCAGCAGGAGCGGGATGAGCTGGCTGACGAGATCGC  5132

Qy  372   uAsnSerPheArgArgAlaProLeuArgLeuSer------------------  383
                   |||||      :::
Db  5133  CAACAGCAGCGTGCCCAAAGAGCCCTGCGTTAGAGAGAAGACGCGGCGTCTGGAGGCCCGCAT  5192

Qy  384   -SerGlyPheValGluLysGluLysLysSer---------  395
                   ::: |||||:::||:|||        ||
Db  5193  CGCCCAGCTGGAGGAGAGCTGGAGGAGCAGGCAACACGAGCTGATCAACGACCG  5252    AsnAspGl  395

Qy  395   uLeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLysTyrLeuAl  415
                   |||:||
Db  5253  GCTGAAGAAGGCC----------AACCTGCAGATCGACCAGATC--------  5286

Qy  415   aProLysProMetGluPheAsnProLysProGlyTyrPheAlaProArgLysIl  435
                   |||||| :: |||
Db  5287  --------------------AACAC-CGACCTGAACCTGGA  5306

Qy  435   eProThrArgProArgLysMetLeuProLeuLeuIleGlySerAspProLysValGlnGl  455
                   :::::||||||
Db  5307  ---GCCAGCCACGCCC-AGAAGACGAGAATGCTCGGCCAGCAGCTGGAACGCCAGAAC  5361

Qy  455   uGluIleLeuArgArgHisProSerThrGluThrLysIleAlaLysGluSerArgValLeuTh  475
                   |||||     |||:|||
Db  5362  AAGGAGCTTAAGGTCAAGCTGCAGGAGATGG----------AGGGCCACTGTC  5403

Qy  475   rAsnLeuLysAsnAsnProSerLeuAlaAlaLeu------------PheMetAspAsp  490
                   |||||
Db  5404  AAGTCC-AAGTACAACAAGGCCTCCATCACCGCCCTCGAGGCCCAAGATTGCACCAGCTGGAGGA  5462

Qy  490   pLysLeuGluAsnThrLeuLysGlyArgGlnMetLeuThrAspGluGlnLysGlyArgTh  510
                   ::||:||::|  |||     ||
Db  5463  GCAGCTGGACAACGAGACCAAGGAGACCAAGGAGGCGCCAGCCTGC---AAACAGGTGCGTCGGAC  5519

Qy  510   rArgValLys  513
                   ||||
Db  5520  CGAGAAGAAG  5529
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```
Qy  15   IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaAlaLeuLeuSer  34
                ...
Db  562  GTGGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGTTG----------  603

Qy  35   SerLeuValGlyLysSerHisGlnLysProLeuAlaProSerMetGluAlaLeuGlu  54
                |||||| ::: :::
Db  604  ---CTTCAAGAAGAAACCCGGCAGAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG  660

Qy  54   ----  54
Db  661  GAGGAGGGGAACAGCCTGCAAGACCAGCCTGGACGAGGAGGATGAGGCGCCAAGCAGAGAACCTG  720

Qy  55   -----LeuMetGlyValGlnPheValAsnAlaAspAlaLeuLeuLysLysGlyGln  69
                ||||:|
Db  721  GAGCGGCCACATCCCACTCTCAACATCCAGCTCTCCGACTCGAAG---AAGAAGCTGCAG  777

Qy  70   ----MetGluMetAlaGlyAlaPheLysThrGlnLeu  81
                ::::   :::::
Db  778  GACTTTGCCAGCACCGTGGAAGCTCTGGAGAGGGAAGAAGAGAGGTTCCAGAAGGAGATC  837

Qy  82   GluValLeuGluLysValHisProAspGln-------PheAspLysTyrLysLysLeu  98
                ||||||:::  ::: :::::
Db  838  GAGAACCTCACCCAGCAGTACGGAGGAGAAGGCGGCCCGCCTTATGATAAACTGGAAAAGACC  897

Qy  99   Lys----------ValAspAspAlaAlaAspAlaValMetGlnGlnAla  112
                |||||
Db  898  AAGAACAGGCTTCAGCAGAGGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA  957

Qy  113  GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn  132
                :::::| |||:::  |||
```

```
RESULT 4
US-08-533-306A-5
; Sequence 5, Application US/08533306A
Patent No. 5837457
GENERAL INFORMATION:
  APPLICANT: Liu, Pu
  APPLICANT: Collins, Francis S.
  APPLICANT: Siciliano, Michael J.
  APPLICANT: Claxton, David
  TITLE OF INVENTION: Markers for Detection of Chromosome 16
  TITLE OF INVENTION: Rearrangements
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
    STREET: P.O. Box 828
    CITY: Bloomfield Hills
    STATE: MI
    COUNTRY: USA
    ZIP: 48303
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
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```
Qy  439  ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysValGlnGluIleIle  457
                                          :::
Db 1973  CCCAGAGAATGAGAGTGCCC------GGCAGCAGCTCGAGCCGGCAGAACAAGGAGAGC    2023

Qy  458  ArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeu  477
                                        ||||||  |||
Db 2024  TCCGGAGCAAGCTCCACGAGATGGAGGG-GCCGTCAAGTCC-----------------    2064

Qy  478  LysAsnAsnProSerLeuAlaAlaLeu------PheMetAspAspLysLeu           492
                            ::::||||||||    ::::::||||||||
Db 2065  AAGTTCAAGTCCACCATCGCGGCGTCTGGAGGCCAAGATTGCACCAGCTGGAGGAGCAGGTC 2124

Qy  493  GluAsnThrLeuLysGlyArgGlnMetLeuThr-                            503
                                              :::
Db 2125  GAGCAGGAGGCCAGAGAGAAACAGGCAGCCACCAAGTCGCTGAAGCAGCAAAGACAAGAAG  2184

Qy  504  ----------------------------------AspGlu                      505
                                           ||||||
Db 2185  CTGAACGGAAAATCTTGCTGCAGGTGAGGACCAGCAGATGGCCAAGATGACGTACAACGAG  2244

Qy  506  ------GlnLysGlyArgThrArgValLysThrIleArgAlaLeuArgLeuPheGly     523
                  :::||||||||    ::::::||||||
Db 2245  CAGGCAGAGAAAGGCAATGCCAGGGTCAAGCAGCTCAAG--------AGGCAGCTGGAG    2295

Qy  524  AlaProThrAlaLysAlaGluMetIleAspAla------LysValPheGlnAsnIle     540
                  ::::||||||||
Db 2296  GAGGCAGAGGAGGAGGTCCCAGGCCATCAACGCGCAGCCCACCGCTGCGCGGGGAGCTG    2355

Qy  541  GluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThrArgLeuArg  560
                                            :::||
Db 2356  GATGAGGCC                                                     2364

Qy  561  TrpThrGlyAlaAsnGlu----------LysGluIleProGlyLeuGlySerArgPheIle 577
                  :::|||||  :::||
Db 2365  ---ACGGAGCAACGAGGCCATGGCCGTGAGGTGAACGCACTCAAGAGCAAGCTCAGA     2421

Qy  578  LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg  597
                                          ::::::||||||||
Db 2422  GGGCCCCCC----CCACAGGA-AACTTCGCGTAGTGATGCACCCAGGCGGAGG         2465

Qy  598  AlaArgAspGluTrpAspThrMetPheLysIle                             608
                  :::||::||
Db 2466  AAACGAGACCTCTTTCGTTCCTTCCTTCTAGAAGGTC                         2498
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Db  958  CTCGTGTCCAACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTCGTTAGCCGAG 1011

Qy  133  GlyIleProIleGlySer                                            139

Db 1012  GAGAAAAACATTCTCTTCCAAATACCGGATGAGAGGACAGAGCTGAGGCAGGAAGCCAGG   1071

Qy  140  ----------IleArgGlyLeuGluAspAlaIleArgThrGln                   150
                            |||  ||||||:::::
Db 1072  GAGAGAGAAACCAAGGCCCTGTCCCGGCTGGAAGAGGCCTTGGAAGCCAAA           1131

Qy  151  ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe  170
                  :::::||||||   ||:::
Db 1132  GAGGACTGCGAGGCCAC----AAAATGCTCAAAGCCCAAATGAA-----            1176

Qy  171  GlnThrGlnIleLeuLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe- 189
                                              ||||||
Db 1177  -------------------GACTTGGTCAGCTCCAAGGATGACGTGGGC            1206

Qy  190  LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla  209
                  |||:::  ||:::
Db 1207  AAGAACTTCCATGAGCTGGAGAAGTCCAAGCTGGAGGACCCCAGATGGGAGGAGATG     1266

Qy  210  LeuAlaGlnIleArgAlaMetLeuGlyLysAsnAlaProValAlaGlyValArgGlyGluGlu 229
                  |||                                 :::
Db 1267  AAGACCAGCTGGAAGAGCTGGAAGAGCGAGCTGCAAGCCTG-------GAGGAC       1314

Qy  230  GlnArgMetMetAsnArgValAspGlnMetGln------------------Gln       243
                  :::::||
Db 1315  GCCAAACTG----------CGGCTGGAAGTCAACATGCAGGCGCGTCAAGGGCCAGTTCGAA 1365

Qy  244  ArgGluLeuGlnGluGlnLysLysAspAspAspAspLeuGluGluAspValProArg     263
                  |||||:::|||||
Db 1366  AGGGATCTCCAAGCCCGGGACGAGCAGAATGAGGAG---------------AAG        1404

Qy  264  ArgArgSerSerAsp---------GlyGluProGlnSerGluAlaGluHisGlnArgArg  280
                  |||||   ||:::
Db 1405  AGGAGGCAACTGCAGAGACAGCTTCACGAGTATGAGACGGGACTGAAGACGAGCGAAAC   1464

Qy  281  AspLeuAlaArgArgLeuLysSerSerProArgLeuGluLysSerProLeuGluLeuGlnAsnAlaGlu 300
                  :::|||
Db 1465  GAACGTGCCCTGGCAGCTGCGCAAAGAGCAGAAGTCTGGAGCGGGCACCTGAAAGACCTGGAG 1524

Qy  301  ValGlnSerLeuLeuSerTyrGlnArgMetArgMetAspSerProLeuSerArgArgPro  320
                  ::::||||||
Db 1525  CTTCAGGCC----GACTCTGCCATCAAGGGAGGAGGAGCAAGCCATCAAGCAGCTACGCAAA 1581

Qy  321  Leu------AlaMetAsnAsp--------------GluAspGluSerAlaPheArg------ 332
                  |||||||
Db 1582  CTGCAGGCTCAGATGAAGGACTTTCAAAGAGAGCTGAGATGCCCGTGCCTCCAGAGAT    1641

Qy  333  AlaMetGluAlaArgAlaLysAlaLeuAspLysLeuLysSerGlnLysLeuValLeuGluValLeuGlnGlyLeuHisGlyGly 352
                  |||   |||      :::||
Db 1642  GAGATCTTTGCCACAGCACTCGCAGACAGCAATGAGAAGAAGCCAAGAGCTTG--------  1689

Qy  353  PheGlyGlySerAspAspAspAspAspAspGluLeuAspProProSerGluProSerGlu  372
                  ||:::||||
Db 1690  -----GAAGCAGACCTCATGCAGCTACAAGAGGAC----CTCGCCGCCGCCTGAG       1734

Qy  373  AsnSerPheArgArgAlaProLeu----------ArgLeuSerGlyPheValGluLysLys 389
                  ::: :::||::
Db 1735  AGGGCTCGCAACAAGCCGACCTGCAGAAGAGGACTTGCCAGAGAGCTGGCCAGTAGC    1794

Qy  390  LeuLysSerAsnAspSerGluAspLeuLeuLysSerAlaLeuAspArgIleLysLysTyrArgValAspAsp 409
                  |||||:::
Db 1795  CTGTCGGAAGGAACGACACTCCAGAGACGAGAAGCGCCGCCTGGAGGCCCGGATCGCCCAG  1854

Qy  410  ValGluTyrLeuLysAlaProLeuProLysProMetGluPheAsnProLysProGlyTyr  429
                  ::::|||  |||:::
Db 1855  CTGGAGGAGGAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGGAGCCGACCCGGTCC- 1912

Qy  430  PheAlaProArgLysIleProThr--------------------------Arg         438
                  |||
Db 1913  GCAAAGCCACACAGCAGCCCGACGCAGCTCAGCAACGAGCTGGCCACAGAGCGCCAGCACGG 1972
```

```
;  ATTORNEY/AGENT INFORMATION:
;     NAME:  Smith, DeAnn F.
;     REGISTRATION NUMBER:  36683
;     REFERENCE/DOCKET NUMBER:  2115-00869DVC
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (810) 641-1600
;     TELEFAX:   (810) 641-0270
; INFORMATION FOR SEQ ID NO: 5:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:  2680 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;     ORGANISM:  Homo sapiens
;     INDIVIDUAL ISOLATE:  Sample 2
;     TISSUE TYPE:  Acute myelomonocytic leukemia, M4Eo
;     TISSUE TYPE:  subtype (inv16)
;    POSITION IN GENOME:
;     CHROMOSOME/SEGMENT:  16[inv(16) (p13q22)]
;    FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  1..2451
US-08-742-923A-5

Alignment Scores:
Pred. No.:            3.08e-06       Length:          2680
Score:               159.00         Matches:          150
Percent Similarity:   38.3%         Conservative:     130
Best Local Similarity: 20.5%        Mismatches:       230
Query Match:           4.8%         Indels:           225
DB:                                 Gaps:               2

US-10-736-868-2 (1-643) x US-08-742-923A-5 (1-2680)

Qy    15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaAlaLeuSer 34
Db   562 GTGGCGTGCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGTTG---------------- 603

Qy    35 SerLeuValGlyLysSerHisGlnLeuGlnLeuProLeuAlaProSerMetGluAlaLeuGlu 54
Db   604 ---CTTCAAGAGAAACCCGGCAGAGCTCAACGTGTCTACCGAAGCTGCCGCCAGCTGGAG 660

Qy    54 --------------------------------------------------------- 54
Db   661 GAGGAGGCGGAACAGCGCTGCCAAGCACCAGCTGGACGAGGAGATGGAGGCCAAGAACCTG 720

Qy    55 --------------LeuMetGlyValValGlnPheValAspProSerGln------- 69
Db   721 GAGGCGCCACATCCACACTCCAACATCCAGCTCTCCAGCTGCGAAG---AAGAAGCTGCAG 777

Qy    70 --------------MetGluMetAlaLysGlyLysGlyLysGluLysGlyThrGlnLeu 81
Db   778 GACTTTGCCAGCACCGTGGAGCTCTGGAAGAAGGAAGAGAGGTTCCAGAAGGAGATC 837

Qy    82 GluValLeuGluLysValHisProAspGln--------PheAspLysTyrLysLysLeu 98
Db   838 GAGAACCTCACCGAGCAGTACCAGGAGGAGGCGGCCCTTATGATAAACTGGAAAAGACC 897

Qy    99 Lys------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla 112
Db   898 AAGAACAGGCTTCAGCAGGAGGAGCTGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA 957

Qy   113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspAspMetLeuAsnGlyAsn 132
Db   958 CTCGTCTCCAACCTGGAAAAGAGAGCAGAGAAA------TTTGATCAGTTGTTAGCCGAG 1011

Qy   133 GlyIleProGlySerSer-------------------------------- 139
Db  1012 GAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAGCTGAGGCGAGAAGCCAGG 1071

Qy   140 -----------------------IleArgGlyLeuGluAspAlaIleAlaArgThrGln 150
Db  1072 GAGAAGGAAACCAAGGCCCTGTCCTGGCTCGGGCCCTTGAAGAGCCCAA 1131

Qy   151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaAlaValMetAspLysPhe 170
Db  1132 GAGGAACTCGAGCGACCAAC---AAAATGCTCAAAGCGAAATGGAA----- 1176

Qy   171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
Db  1177 -----------GACCTGGTCAGCTCCAAGGATGACGTGGGC 1206

Qy   190 LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
Db  1207 AAGAAACGTCCATGAGCTGGAGAAGTCCAAGCGGCCCTGGAGACCCGAGATGGAGGAGATG 1266

Qy   210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyArgGlyGlu 229
Db  1267 AAGACGCAGCTGGAAGACGTGGAGGACGAGCTGCAAGCCTCG---------GAGGAC 1314

Qy   230 GlnArgMetMetMetAsnArgValAspGlnArgMetGln-------------Gln 243
Db  1315 GCCCAAACTG-----CGGCTGGAAGTCAACATGCAGCGAGTGGACCGGCGGCTCAAGGCGCCTCAAGGGCACGTTCGAA 1365

Qy   244 ArgGluLeuGlnGluGluGlnAlaProProGluLeuGluAspGluGluGluAspSerValProAspValProArg 263
Db  1366 AGGGATCTTCCAAGCCCGGGACGACGCAGAATGAGGAG----------------AAG 1404

Qy   264 ArgArgSerSerAsp----------GlyGluProGlnSerGluGlnGlnHisGlnArgArg 280
Db  1405 AGGAGGCAACTGCAGAGACAGCTTCACGATGAGACGGACTTGGAAGACGAGCGAGCGGAAAC 1464

Qy   281 AspLeuAlaArgArgLeuLysSerSerProArgLeuLysSerGluLysGlnLeuAsnAlaGlu 300
Db  1465 GAACGTGCCCTGCAGCTGCAGCAAAGAAGAGAGCTGAAGGGGACCTGAAAGACCTGGAG 1524

Qy   301 ValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgPro 320
Db  1525 CTTCAGGCC---GACTCTGCCATCAAGGGAGGGAGGAAGCCATCAAGCAGCTACGCAAA 1581

Qy   321 Leu------AlaMetAsnAsp------------GluAspGluSerAlaPheArg 332
Db  1582 CTGCAGGCTCAGATGAAGGAGACTTTCAAAGAAGAGATGCCCGTGCCTCCAGAGAT 1641

Qy   333 AlaMetGluAlaArgAlaLysLysAspAspArgIleLysSerArgLeuLysGlyLysHisGly 352
Db  1642 GAGATCTTTGCCACCAGCGCCCAAGAGAATGAGGAGAGAAAGCCAAGGAGTTG------- 1689

Qy   353 PheGlyGluSerAspAspAspGluGluAspGluAspAspGluAsnLeuIleLeuAspProSerGlu 372
Db  1690 -----GAAGCAGACCTCATGCAGCTACAAGAGGAC---------CTCGCCGCCGCTGAG 1734

Qy   373 AsnSerPheArgArgAlaProLeu-----------ArgLeuSerSerGlyPheValGluLys 389
Db  1735 AGGGCTCGCAAACAAGGGGACCTCGAGAAGGAGAGCTGGCAGAGGACTGGCCAGTAGC 1794

Qy   390 LeuLysSerAsnAspAspGluLeuLysSerAlaLeuArgIleLysTyrArgValAspAsp 409
Db  1795 CTGTCGGGAAGGAAGACCACTCCAGGACCCGAGGGCCGGATCGCCCAG 1854

Qy   410 ValGluLysTyrLeuAlaProLysProMetGluPheAsnProLysProGlyTyr 429
Db  1855 CTGGAGGAGGCTGGAGGAGGACAGG-CAACATGAGGCCATGAGCGACCGGGTCC-- 1912

Qy   430 PheAlaProArgLysIleProThr-----------------Arg 438
Db  1913 GCAAAGCCACACAGCAGGCCACAGCTCAGCAACCAGCTGCCACAGCCAGCACGG 1972

Qy   439 ProArgLysMet---LeuProLeuLeuGluLeuGlyLeuSerAspProLysProLysValGlnGlnIle 457
Db  1973 CCCAGAGAATGAGAGTGCCC-------GGCAGCAGTCGAGCGGCGGCAGAACAAGGAGC 2023
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Qy    458  ArgArgHisProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeu  477
                ||||||      |||:|||          ||:|||
Db   2024  TCCGGAGCAAGCTCCACGAGATGGGAGGGG-GCCGTCAAGTCC------           2064

Qy    478  LysAsnAsnProSerLeuAlaAlaLeu-----------------PheMetAspAspLysLeu  492
                |||:||||                           :::::::|||||||
Db   2065  AAGTTCAAGTCACCATGCGCGGCCGGCCTGGAGGCCAGCTGCACAGCTGGAGGAGCAGGTC  2124

Qy    493  GluAsnThrLeuLysGlyArgGlnMetLeuThr-----------------           503
                |||   ::    ||:|||
Db   2125  GAGCAGGAGGCCAGAGAGAAACAGGCAGCCACCAAGTCGCTGAAGCAGAAGACAAGAAG    2184

Qy    504  ------------------------------------AspGlu-----------           505
                                                    |||||
Db   2185  CTGAAGGAAATCTTCGTGCAGTGGAGGACGCGCAAGATGGCCGAGCAGTACAAGGAG    2244

Qy    506  -----GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly    523
                   ::|||||||       ||||||||  :::::           |||
Db   2245  CAGGCAGGAAGGCAATGCCAGGCTCAAGCAGCTCAAG--------AGGCAGCTGGAG    2295

Qy    524  AlaProThrAlaLysAlaAlaGluMetIleAspAla--------LysValPheGlnAspIle    540
                :::|||      |||:||  |||:|||
Db   2296  GAGGCAGAGGAGGAGTCCAGCCATCAACGCCCAACGCCAGGAAGCTGCAGCGGGAGCTG    2355

Qy    541  GluGluArgProIleProLeuPhePheGluProLysGlyArgGlyArgHisThrArgLeuArg   560
                ::||             |||||
Db   2356  GATGAGGCC----------------------------------           2364

Qy    561  TrpThrGlyAlaAsnGlu--------LysGluIleProGlyLeuGlyGlySerArgPheIle   577
                   :::||||||              |||:|||
Db   2365  -ACGGAGCGAGGAGGAGGACCCGTGAGGTGAACGACGTCAAGAGCAAGCTCAGA    2421

Qy    578  LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg    597
                ||:||                   :::
Db   2422  GGGCCCCCC-------------------CCACAGGA-AACTTCGCAGTGATGCACCAGGCGAGG  2465

Qy    598  AlaAlaArgAspGluTrpAspThrPheLysIle    608
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Db   2466  AAACAGGAACCTCTTTCGTTCCTTCTTAGAAGGTC    2498
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RESULT 6
US-08-533-306A-3
; Sequence 3, Application US/08533306A
; Patent No. 5837457
GENERAL INFORMATION:
;   APPLICANT: Liu, Pu
;   APPLICANT: Collins, Francis S.
;   APPLICANT: Siciliano, Michael J.
;   APPLICANT: Claxton, David
;   TITLE OF INVENTION: Markers for Detection of Chromosome 16
;   TITLE OF INVENTION: Rearrangements
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
;   STREET: P. O. Box 828
;   CITY: Bloomfield Hills
;   STATE: MI
;   COUNTRY: USA
;   ZIP: 48303
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/533,306A
;   FILING DATE: September 25, 1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, DeAnn F.
;   REGISTRATION NUMBER: 36683
;   REFERENCE/DOCKET NUMBER: 2115-00869COB
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (810) 641-1600
;   TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2887 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;   INDIVIDUAL ISOLATE: Sample 1
;   TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
;   TISSUE TYPE: subtype (inv16)
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT: 16(inv(16) (p13q22)]
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..2658
US-08-533-306A-3

Alignment Scores:
Pred. No.:                3.46e-06          Length:         2887
Score:                    159.00            Matches:         150
Percent Similarity:       38.3%             Conservative:    130
Best Local Similarity:    20.5%             Mismatches:      230
Query Match:              4.8%              Indels:          225
DB:                       2                 Gaps:             35

US-10-736-868-2 (1-643) x US-08-533-306A-3 (1-2887)

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Qy     15  IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaAlaLeuLeuSer   34
                :::||||                      |||
Db    769  GTGGGCGTCCCTCAGTTCCCAGCTCAGACACCCAGGAGTG-                 810

Qy     35  SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu    54
                ||||               :::::::||||||        :::
Db    811  ---CTTCAAGAGAAACCCGGCAGAAGCTCAACGTGTCTCACGAAGCTGCGCCAGCTGGAG   867

Qy     54  ---------------------------------------------------------  54
Db    868  GAGGAGCGGAACAGCTGCAAGACCAGCTGCAAGAGGAGATGGGAGGCCAAGCAGAACCTG  927

Qy     55  -------------------------LeuMetGlyValGlnPheValAspAlaLeuIleLysGlyGln    69
                                         :::||          |||||
Db    928  GAGCGCCACATCTCCACTCTCAACATCCAGCTGCCACTCGAAG---AAGAAGCTGCAG   984

Qy     70  -------------------------------MetGluMetAlaLysGlyAlaPheLysThrGlnLeu    81
                                               ::|||     |||||       :::::::
Db    985  GACTTTGCCAGCACCGTGGAAGCTCTGGAGGAGAGGGGGGAAGAGAGGTTCCAGAAGGAGATC   1044

Qy     82  GluValLeuGluLysValHisProAspGln-----------PheAspLysTyrLysLysLeu    98
                |||||||           :::           :::|||
Db   1045  GAGAACCTCACCCCAGCAGTACCGAGGAGAAGGCGGCCGCTTATGATAAACTGGAAAAGACC   1104

Qy     99  Lys-----------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla   112
                |||                :::||
Db   1105  AAGAACAGGCTTCAGGAGGACTGGACGACCTGGTTGGTTGTTGGACAACCAGCGGCCAA   1164

Qy    113  GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn    132
                :::::::|||:|||          ||||||       ::
Db   1165  CTCGTGTCCACCTGGAAAAGAAGCAGAGGAAA------TTTGATCAGTTGTTAGCCGAG    1218

Qy    133  GlyIleProIleGlySerSer---------------------------------    139
                :::|||||||
Db   1219  GAGAAAAACATCTTCTCCAAATACGCGGATGAGAGGGACAGCTGAGCGCAGAAGCCAGG    1278

Qy    140  -----------------IleArgGlyLeuGluAspAlaIleArgThrGln    150
                                 |||||||    |||:::
Db   1279  GAGAAGGAAACCAAGGCCCCTGTCCCTGGCTCGGGCCCTTGAAGAGCCAAA    1338
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Qy  151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysValMetAspLysPhe 170
            :::::| |||| :::::: |||||| ::::
Db 1339 GAGGAACTGAGCGGACCACAC------AAAATGCTCAAAGCCGAAATGGAA------ 1383

Qy  171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
                        ||||| | :::::| ||||:||
Db 1384 ------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 1413

Qy  190 LysMetProGlnMetArgArgLysAlaGlnAlaAlaProSerValPheGlnGlnAla 209
            ||| ::::::| ||||
Db 1414 AAGAACCGCCATGAGCTGGAGAGTCCAAGCGGCCCTGGAGACCCAGATGGAGGAGATG 1473

Qy  210 LeuAlaGlnArgAlaMetLeuGlyLysLysAsnAlaProValAlaGlyGlyArgGlyGlyGlu 229
            :::
Db 1474 AAGACCGGCAGTGGACGAGCTGGAGGACGCAGCCTCG------GAGGAC 1521

Qy  230 GlnArgMetMetMetAsnArgValValAspProGlnArgMetGln----------Gln 243
            ||||||||| :::::|
Db 1522 GCCAAACTG------------CGGCTGGAAGTCAACATGCAGGCGGCCTCAAGGGCCAGTCGAA 1572

Qy  244 ArgGluLeuGlnGluGlnAspAspAspLeuGluAspProGluAspGlyValProArgArg 263
            ||||||||||| :::::::
Db 1573 AGGGATCTCCAAGCCCGGGACCAGCAGAATGAGGAG----------AAG 1611

Qy  264 ArgArgSerSerAsp--------GlyGluProGlnSerGluAlaGluHisGlnAsnArgArg 280
            ||||||
Db 1612 AGGAGGCAACTGCAGAGACCAGCTTCACGAGTATGAGCAACGACGAGCCGAAAC 1671

Qy  281 AspLeuAlaArgArgLeuLysSerProGlyLeuLeuGlnLeuGlnAsnAlaGluGlu 300
            :::::::::
Db 1672 GAACGTGCCCTGGCAGCTGCAGCAAGAGAAGCTGAAAGACCTGGAG 1731

Qy  301 ValGlnSerLeuLeuSerGlnTyrGlnArgMetArgAspSerProLeuSerArgArgPro 320
            :::|||||| :::::| |||
Db 1732 CTTCAGGCC---GACTCTGCCATCAAGGGAGGGGACGGAAGCCATCAAGCAGCTACGCAAA 1788

Qy  321 Leu------AlaMetAsnAsp------------------------GluAspGluSerAlaPheArg--- 332
            ||| |||||||
Db 1789 CTGCAGGCTCAGATGAAGGACTTTCAAAGAGAGCTGGAAGATGCCGTGCCTGCCTCCAGAGAT 1848

Qy  333 AlaMetGluAlaAlaArgAlaAlaLysLeuAspAspGlyLysLysSerGlnAsnLeuValLeuGlyLeuHisGly 352
            :::|||
Db 1849 GAGATCTTTGCCACAGCCAAGAGAATGAGAGAGAAAAGCCAAGAGCTTG---------- 1896

Qy  353 PheGlyGluSerAspAspAspAspGluGluAspProGluGluAspAspAsnLeuLeuAspProSerGlu 372
            :::|||||||
Db 1897 ------GAAGCAGACCTCATGCAGTCTACAAGGAGGAC------CTCGCGCCGGCCTGAG 1941

Qy  373 AsnSerPheArgArgAlaProLeu--------ArgLeuSerSerGlyPheValGluLys 389
            ::: |||||
Db 1942 AGGGCTCGCAAACAAGCGGACCTCGAGAGGAGGACTGGCCAGGAGAGCTGGCCAGTAGC 2001

Qy  390 LeuLysSerSerAsnAspGluLysSerGluSerAlaLeuAspAspArgIleLeuLysValTyrArgValAlaAspAsp 409
            :::::| |||
Db 2002 CTGTCCGGAAGGAAGCCACACTCCAGGCACGAGAGCGCCGCCCTTGGAGCCCGGACCCAG 2061

Qy  410 ValGluLeuLysTyrLeuAla--------LeuProLeuAlaProLysAspProMetGluProGluAsnProLysProGlnProGlyTyr 429
            ::::| :::
Db 2062 CTGGAGGAGGACTGAGAGGAGGAGGATGAGGTGGAGGGGCGGCAGAACAAGGAGC 2119

Qy  430 PheAlaProArgLysIleProThr--------Arg 438
            ||| ::::::
Db 2120 GCAAAGCCACACAGCCCCAGCCAGCTCTGCCACCAGAGCGCAGCACGG 2179

Qy  439 ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIle 457
            ||||||:::::||| :::
Db 2180 CCCGGAGAATGAGACGTGCCC------GGCAGCAGCTCGAGCGGCAGAACAAGGAGC 2230

Qy  458 ArgArgHisProSerThrGluTrpLysIleLysAlaLeuAlaLysGluSerArgValLeuThrAsnLeu 477
            :::::|
Db 2231 TCCGGCAGCAAGCTCCACGAGTATGAGGGG-GCCGTCAAGTCC--- 2271

Qy  478 LysAsnAsnProSerLeuAlaAlaLeu------------PheMetAspAspLysLeu 492
            |||
Db 2272 AAGTTCAAGTCCACCATCGGCGGCGTCCTGGAGCGCTGGAGATTGCACAGCTGGAGGAGCAGGTC 2331

Qy      GluAsnThrLeuLysGlyArgGlnMetLeuThr--- 503
            ||| ::: |||
Db 2332 GAGCAGGAGGCCAGAGAGAAACAGGCACCAAGGTCGCTGAAGCAAGTCGCTGAGACAAGAAG 2391

Qy  504 AspGlu--- 505
            |||
Db 2392 CTGAAGGAAATCTTGCTGCAGGTGGAGGAGGCGCAAGATGCCGAGCAGTACAAGGAG 2451

Qy  506 -----GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly 523
            :::||||
Db 2452 CAGGCAGAGAAGGCAATGCCCAGGGTCAAGCAGCTCAAG------AGGCAGTCGGAG 2502

Qy  524 AlaProThrAlaLysValAlaGluMetIleAspAla--------LysValPheGlnAspIle 540
            :::::::||| :::::
Db 2503 GAGGCAGGAGGAGGAGTCCCAGCGCATCAAGCCCAACCGCAGGAAGTCGCGGCGGGAGCTG 2552

Qy  541 GluGluGlnArgProIleProProLeuPheGluProArgLysGlyArgHisThrArgLeuArg 560
            ::::::||||||
Db 2563 GATGAGGCC---------------------- 2571

Qy  561 TrpThrGlyAlaAsnGlu--------------LysGluIleProGlyLeuGlySerArgPheIle 577
            ||| :::::||||
Db 2572 ---ACGGAGAGCAACAGGGCCGTGAGTGGTGAAGCACTCAAGGAGCAAGCTCAGA 2628

Qy  578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg 597
            :::|||||||
Db 2629 GGGCCCCC--------CCACAGGA-AACTTCGCGATGTGATGCACCAGGAGGAGG 2672

Qy  598 AlaArgAspGluTrpAspThrMetPheLysIle 608
            |||
Db 2673 AAACGAGACCTCTTTCGTTCCTTCTTTCTAGAAGGTC 2705

RESULT 7
US-08-742-923A-3
; Sequence 3, Application US/0874292 3A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT:  Liu, Pu
; APPLICANT:  Collins, Francis S.
; APPLICANT:  Siciliano, Michael J.
; APPLICANT:  Claxton, David
; TITLE OF INVENTION:  Markers for Detection of Chromosome 16
; TITLE OF INVENTION:  Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY:  Bloomfield Hills
; STATE:  MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,923A
; FILING DATE: No. 5869611ember 1, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME:  Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX:  (810) 641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2887 base pairs

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;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;       MOLECULE TYPE: cDNA to mRNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;         ORGANISM: Homo sapiens
;         INDIVIDUAL ISOLATE: Sample 1
;         TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
;         TISSUE TYPE: subtype (inv16)
;       POSITION IN GENOME:
;         CHROMOSOME/SEGMENT: 16[inv(16) (p13q22)]
;       FEATURE:
;         NAME/KEY: CDS
;         LOCATION: 1..2658
; US-08-742-923A-3

Alignment Scores:
Pred. No.:             3.46e-06     Length:        2887
Score:                 159.00       Matches:        150
Percent Similarity:    38.3%        Conservative:   130
Best Local Similarity: 20.5%        Mismatches:     230
Query Match:           4.8%         Indels:         225
DB:                                 Gaps:            35

US-10-736-868-2 (1-643) x US-08-742-923A-3 (1-2887)

Qy     15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaAlaLeuSer   34
             :::|||  |||||||||:::||
Db    769 GTGGCGTCCCTCAGTTCCCAGCTCCAGGACCCCAGGAGTG---                    810

Qy     35 SerLeuValGlyLysSerHisGlnLysSerMetGluAlaLeuProSerMetGluAlaLeuGlu   54
             |||          ::     :::
Db    811 ---CTTCAGAAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCCCCAGCTGGAG    867

Qy     54                                                                  54
Db    868 GAGGAGCGGAACAGCCTGGACAGACGCCTCGAGACGAGCTGGACAGGAGCCAAGCAGACCTG  927

Qy     55       LeuMetGlyValGlnPheValAspAlaAlaLeuIleLysLysGlyGln          69
               :::  :::|||    ||||::::
Db    928 GAGCGGCCACATCTCCACTCTTCAACATCCAGCTCTCCGAAG--AAGAAGCTGCAG       984

Qy     70               MetGluMetAlaLysGlyAlaPheLysThrGlnLeu            81
                        :::|||
Db    985 GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAGAGAGAGGTTCCAGAAGGAGATC 1044

Qy     82 GluValLeuGluLysGlyValHisProAspGln-------PheAspLysTyrLysLysLeu   98
             |||    ::     ::
Db   1045 GAGAACCTCACCCAGTACGGAGGAGAAGAGGCGGCCACCTGGAGAAGGAGATGCCCAG     1104

Qy     99 Lys------------ValAspAspLeuAlaLysAspAlaPheIleLysGlyLys         112
             |||          :::||||||||       ||
Db   1105 AAGAACAGGCTTCAGCAGAGCTGGTTGATTTGGATAATGAAACTGGAAAGACC          1164

Qy    113 GluMetAlaLysGluGlnLysProLysSerGlyAsnAlaPheIleAspPheMetLysAsnGlyAsn  132
Db   1165 CTCGTGTCCAACCTGAAAAGAAGACAGAGGAAA------TTTGATCAGTTGTTAGCCGAG  1218

Qy    133 GlyIleProIleGlySerSer                                          139
             |||
Db   1219 GAGAAAAACATCTCTTCCAAATACGGCGATGAGGAGACGGAGAGTCTGAGGCGAGAAGCCAGG 1278

Qy    140 ------------------IleArgGlyLeuGlnAspAlaIleLeuArgThrGln          150
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Db   1279 GAGAAGGAAACCAAGGGCCCTGCCCTGCCTCGGCGGGGCCCTTGGAAGCCAAA         1338

Qy    151 ArgAspMetGluAsnThrAspProSerGluGlnIleLeuAlaLysAlaValMetAspLysPhe  170
             :::  ||::::  :::
Db   1339 GAGGAACTCGAGCGGACCAAC------AAAATGCTCAAAGCCGAAATGGAA-------     1383

Qy    171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysLysAsnPhe---    189
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Db   1384 ------------------------------GACCTGGTCAGCTCAGCTGACGATGACGTGGGC 1413

Qy    190 LysMetProGlnMetArgLysArgAlaGlnAlaAlaAlaProSerProValPheGlnGlnAla  209
             |||      :::   ::     ||||
Db   1414 AAGAACGTCCATGAGCTGGAGAAGTCCCTGGAGACCCAGATGAGGAGGATG           1473

Qy    210 LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyLysArgGlyArgGlyGlu  229
             |||||||
Db   1474 AAGACGCAGCTGGAAGACTGGAGAGCAGCTGCAAGCCTCG------GAGGAC          1521

Qy    230 GlnArgMetMetMetAsnArgValAspValAspArgMetGln----                 243
             :::|||
Db   1522 GCCAAACTG-------CGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTCGAA     1572

Qy    244 ArgGluLeuGlnGluGluLysProAspAspAspAspAspLeuGluAspGluValProArg    263
             |||||||||:::
Db   1573 AGGGATCTCCAAGCCCCGGACGAGCAGAATGAGGAG                          1611

Qy    264 ArgArgSerSerAsp---------GlyGluProGlnSerGluAlaGluGlnHisGlnArgArg  280
             |||||||
Db   1612 AGGAGGCAACTGCAGAGACAGTTCACGAGTATGAGGACACTGGAGACGGAAC          1671

Qy    281 AspLeuAlaArgArgLeuLysSerSerProArgLeuLysGluLeuLeuGlnAsnAlaGlu    300
             :: ||||||
Db   1672 GAACGTGCCCTGGCAGCTGCAGCAAGAAGAAGAGAGCTGGAAGGGGACCTGAAAGACTTGGAG 1731

Qy    301 ValGlnSerLeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgPro    320
             :::|||:::    |||   ::: |||
Db   1732 CTTCAGGCC---GACTCTGCCATCAAGGGAGGAGGAGAGGAGCCATCAAGCAGTACCGCAAA  1788

Qy    321 Leu-----AlaMetAsnAsp-------------GluAspGluSerAlaPheArg----     332
             |||                           :::
Db   1789 CTGCAGGCTCAGATGAAGGACTTTCAAGACAGCTTGAAGATGCCCCTGCCTCCAGAGAT    1848

Qy    333 AlaMetGluAlaArgAlaLysAspAlaLeuAsnLysSerGlnLysLeuLeuGlyLeuHisGly  352
             |||
Db   1849 GAGATCTTTGCCACAGCCAAGAATGAGAAGAAAGCCAAGAGCTTG---              1896

Qy    353 PheGlySerAspAspAspAspAspLeuGluAspGluLeuAsnLeuIleLeuAspProSerGlu  372
             :::  ||||                :::|||
Db   1897 ------GAAGGAGACCTCATGCAGCTACAAGAGGAC------CTCCGCCCGCTGAG       1941

Qy    373 AsnSerPheArgArgAlaProLeu------------ArgLeuSerArgSerGlyPheGluValLys 389
             ||                           :::|||
Db   1942 AGGGGCTCGAACAACAAGCAGACCTCGAGAAGGAGGAGCTGGACAGGAGCTGGCCAGTAGC  2001

Qy    390 LeuLysSerAsnAspGluLeuLeuSerAlaAlaLeuAspArgIleLeuLysAspProGlyTyr  409
             |||::::
Db   2002 CTGTCGGGAGGAGAACGCACTCCAGGACGAGAAGGCCGGCCTGGAGAAGGAGATCGCCCAG  2061

Qy    410 ValGluLysTyrLeuValAlaProLeuProLysGluProAsnProLysProGlnIleProGlyTyr 429
             :::||||||
Db   2062 CTGGAGGAGGAGGGCCATGAGCGGCCAGGG-CAACATGGAGCGCGACCGGGTCC--      2119

Qy    430 PheAlaProArgLysIleProThr-------------------------------Arg     438
             :::|||
Db   2120 GCAAAGCCACACAGCCCAGACGCAGCTGCAGCAACAGGCGCCAGCACGG            2179

Qy    439 ProArgLysMet---LeuProLeuLeuIleGlySerAspProLysAspProLysValGlnGluIle 457
             |||||||
Db   2180 CCCAGAAGAATGAGAGTGCCC------GGCAGCAGCTCGAGCGGCAGAACAAGGAGC     2230

Qy    458 ArgArgHisProSerThrGluTrpLysIleAlaAlaLysGluSerArgValLeuThrAsnLeu  477
             ||||||||:::
Db   2231 TCCGGAGCAAGCTCCACGAGATGAAGGGG-GCCGTCAAGTCC---                2271

Qy    478 ------------------------------PheMetAspAspLysLysLeu          492
                                           :::|||
Db   2272 AAGTTCAAGTCCACCATCGCCGCGCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGTC   2331

Qy    493 GluAsnThrLeuLysGlyArgGlnMetLeuThr                             503
             :::  |||
```

Db  2332 GAGCAGGAGGCCCAGAGAGAAACAGGCCAGCCACCAAGTCGCTGAAGCAGAAGACAAGAAG 2391
                              |||||
Qy  504 ------------------------------------------AspGlu----------- 505

Db  2392 CTGAAGGAAATCTTGCTGCGTGGAGGAGGACGAGCGCAAGATGGCCAGCAGTACAAGGAG 2451
                   |||||
Qy  506 ------GlnLysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGly 523

Db  2452 CAGGGCAGAGAAGGCAATGCCAGGCGTCAAGCAGCTCAAG--------AGGCAGCTGGAG 2502
              |||:|:|||            |||
Qy  524 AlaProThrArgLysAlaGluMetIleAspAla--------LysValPheGlnAspIle 540

Db  2503 GAGGCAGAGGAGGAGGAGTCCCAGCGCATCAACGCCCAACCGCAGGAAGCTGCAGCGGAGCTG 2562
             :|:|::|||
Qy  541 GluGluArgProIleProProLeuPhePheGluProLysGlyArgHisThrArgLeuArg 560

Db  2563 GATGAGGCC---------------------------------------------------- 2571
            :|||
Qy  122 GlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIle--------------------Pro 135

Db  2572 ---ACGGAGAGCAACGAGGCCATGGCCGTGAACGACTCAAGAGCAAGCTCAGA------- 2628
      |||    :::|||||
Qy  561 TrpThrGlyAlaAsnGlu---------LysGluIleProGlyLeuGlyGlySerArgPheIle 577

Db  578 LeuProSerLeuAspProThrMetProAlaLeuAsnThrAlaPheSerThrGlnGlyArg 597
      ||||||
Db  2629 GGGCCCCCC--------------------CCACAGGA-AACTTCGCAGTGATGCACCAGGCGAGG 2672

Qy  598 AlaArgAspGluTrpAspThrMetPheLysIle 608
         |||  :::
Db  2673 AAACAGGAGACCTCTTTCGTTCCTTCTAGAAGGTC 2705

Alignment Scores:
Pred. No.:                 Length: 4935
Score: 8.04e-06          Matches: 159
       159.00            Conservative: 97
Percent Similarity: 36.1%     Mismatches: 260
Best Local Similarity: 22.4%   Indels: 196
Query Match: 4.8%           Gaps: 35
DB: 3

US-10-736-868-2 (1-643) x US-09-949-016-1019 (1-4935)

Qy  23 ProSerThrSerAspAlaProGlyAlaLeuLeuSer--SerLeuValGlyLysSerHis 41
       ||||||||    :::|||
Db  484 CCGAGTACCTCACGCAAGATGCGAGCTGGAGGAGGTGACTCTGGACGGGGAAGCCTCTT 543

Qy  42 GlnLysLeuProLeuAlaProSerMetGluAlaLeuGluLeuMetGlyValGlnPheVal 61
       ||         ||||||||
Db  544 CAGGGCCGCTGCGGGTGACCACGGCCCGACCTGAGCGCCACTGGAGCCAGCGCGAGGC------ 591

Qy  62 AspAlaLeuIleLysLysGlyGln----------------MetGluMetAlaLysGly----- 75
       |||           :::::
Db  592 ------CTAGCCAAGAGACGCGGGAGAAGAGTGCCTGGTCAAGCGGGTCAAAGGGCTCTA 645

Qy  76 ---------------------------------------------AlaPheLysThrGlnLeuGlu 82
                     |||||||
Db  646 ATGCTAGAAATTACAGAAACACTCAACACCCCATGCTGCATTCCAGCCAAATTCCCAG 705

Qy  83 ValLeuGluLysValHisProAspGlnPheAspLysTyrLysLysLeuLysValAspAsp 102
       :::    |||    :::
Db  706 ATTGGTGGAAATGAGCCAGAACAGTTCATAAAACAGTATCTGGAAAAAGCAGCAGGAG 765

Qy  103 LeuAlaAlaAspAlaValMetGlnGlnAla---GluMetAlaLysLeuGlnProLysSer 121
       :::             :::::|
Db  766 CTACTTAGGCACGCGTGGAACGTGGAAGCTCGAGAAGCTGAAGAAGCTTCA 825

Db  826 GCTGAGTCGGAGGACCAGAGATGATCCATCCTGAGGGAGTGGCTTCCCTGCTGCCTCCTGAC 885
                :::
Qy  136 IleGlySerIleArgGlyLeuGluAlaIleIleArgThrGlnArgAspMetGluAsn 155

Qy  156 ThrAspProSerGluGlnIleIleAlaLysAlaValMetAspLysPheGlnThrGlnIleLeu 175
Db  886 TTTCAGACAGCCTGGAGACCAGAGCTGGAGCTCAGCAGCATTCGCCCAGAAAAAGC 945

Db  946 TCCTCAATTTCTGAAGAG-------------------------------------------- 963
        ||||||:|:
Qy  176 ProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPheLysMetProGlnGlnMet 195

Qy  196 ArgLysAlaGlnAlaAlaAlaProSerValPheGlnGlnAlaLeuAlaLeuAlaGlnAlaMet 215
           |||||||     :::               ||||||
Db  964 --------------------------------AAAGGTGACTCTGATGATGAGAAACCA 990
Db  991 AGGAGAAAGGAGAAAGACGCATCATCTAGGGTC---AGACAGGCAAGAGCAGCTAAACTGTCT 1047

Qy  216 LeuGlyLysAsnAlaProValAlaGlyValGlyArgGly------GlnArgMetMe 233
       :::     ||||||||||  ::|||
Db  1048 GAGGGC---AGCCAACCTGCTGA-GGAGGAAGAGGATCAAGAAACACCTTCCAGAAACCT 1103

Qy  233 tMetAsnArgValAspGlnArgMet-----GlnGlnArgGluLeuGlnGluGluAspGl 251
       |||     :::           :::         |||
Db  1104 AAGGGTCAGCAGATCGAAATTTGAAAACAGAGGAGGAAGAGGAGGAGGAGGA 1163

Qy  251 uAspAspAspAspLeuAspLeuAspProArgArgSerArgSerGlyGluPr 271
      |:::::|||          |||
Db  1164 GGAAGAAGATGATGAAGAAGAGGA-----GGTGATGATGAGGG 1202

Qy  271 oGlnSerGluAlaGluHisGlnArgArgLeuAlaArgArgLeuLysSerSerProAr 291
      |||                :::          ::||||
Db  1203 ACAAAAATCTAGGGAG----------------------------GCACCAT 1226

Qy  291 gLeuLysGluLeuLeuGlnAsnAlaGluValGlnSerLeuLeuSerTyrGlnArgMetAr 311
       :::                 :::
Db  1227 CCTGAAAGAGTTTAAGGAAGAAGGGGAA------------------GAGATACCTAGAGTAAA 1271

Qy  311 gAspSerProLeuSerArgProLeuSerArgProLeuAlaMetAsnAspGluAspGlu------ 328
      :         :::             |||||
Db  1272 ACCAGAGGAGATGATGATGAGAACCCAGGAACAGGAGGAGTGTTAGA 1331

Qy  329 ------SerAlaPheArgAlaMetGluAlaArgAlaLysLeuAspArgGlnLysSerGlnLeu 346
               :::            |||:::
Db  1332 GAGAGGAGGGAGGATTTACAAGATCCCAGGAGGAGGCTAGA----AAAAGTCATCT 1382

Qy  346 uValLeuGlyLeuHisGlyPheGlyGluSerAspAspGluAspGluGluAs 366
      |||               :::               |||||
Db  1383 GGCC------------------------------------AGACAGCAGCAGGAGAAGGAAATGAA 1412

Qy  366 nLeuIleAspProSerGluAsnSerPheArgArgAlaProLeuArgLeuSerGlyPh 386
       :::                 |||||
Db  1413 AACAACACTCTCCCCTTGAGGAGGAAGAAGAAGAGAA------ATAAAATCTTCACAAGGCTT 1466

Qy  386 eValGluLeuLysSerAl---------------------------------------AsnAspGluLeuLysSerAl 399
Db  544 CAGGGCCGCTGCGGGTGACCACGGCCCGACCTGAGCGCCACTGGAGCAGCGCGAGGC------

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | | Length: | 4935 |
| Score: | 8.04e-06 | Matches: | 159 |
| | 159.00 | Conservative: | 97 |
| Percent Similarity: | 36.1% | Mismatches: | 260 |
| Best Local Similarity: | 22.4% | Indels: | 196 |
| Query Match: | 4.8% | Gaps: | 35 |
| DB: | 3 | | |

US-10-736-868-2 (1-643) x US-09-949-016-5054 (1-4935)

```
Qy     23  ProSerThrSerAspAlaProGlyAlaLeuLeuSer--SerLeuValGlyAlaLysSerHis   41
               ||||||||||||                         |||
Db    485  CCGAGTACCTCCACGCCAGATGCGGAGTCCTGGAGGAGTGACTCTGGACGGGAAGCCCTCTT  544

Qy     42  GlnLysLeuAlaProLeuAlaProSerMetGlyValLeuGluLeuMetGlyValGlnPheVal   61
               |||                                          ||||||
Db    545  CAGGGCCGCTGCGGGTGACCGACCTGAAGGGCCACTGAGCGAGGC--------------------  592

Qy     62  AspAlaLeuIleLeuLysLysGlyGln------------MetGluMetAlaLysGly-------   75
                                            ||||||          :::::::
Db    593  -----CTAGCCAAGAGCGGGCAGAAGAGTGCCCTGGTCAAGCGGCTCAAGGGGCTCA        646

Qy     76  -----------------------------------------AlaPheLysThrGlnLeuGlu   82
                                                         ||||||    :::
Db    647  ATGCTAGAAAATTTACAGAAACACTCAACACCCCATGCTGCTGCATTCCAGCCAAATTCCCAG  706

Qy     83  ValLeuGlyLysValHisProAspLysPheAspLysIleTyrLysLysLeuValAspAsp    102
               ::: |||                     :::          |||||||
Db    707  ATTGGTGAGGAAATGAGCCAGACAGTTCATAAAACAGTATCTGGAAAAGCAGCAGGAG       766

Qy    103  LeuAlaAlaAspAlaValMetGlnAla--GluMetAlaLysLeuGlnAla------LysSer   121
               ||||                       :::          ||||||:::::::
Db    767  CTACTTAGGCAGCGTCTGGAACGTGAAGCTCGAGAAGCTCGAGAACTTGAAGAAGCTTCA     826

Qy    122  GlyAsnAlaPheIleAspMetLeuAsnGlyAsnGlyIle-----------------Pro    135
               ::: :::                         |||||                  :::
Db    827  GCTGAGTCGGAAGATGATCCATCCTGAGGGAGTGGCTTCCCTGCCTGCCTCCTCGAC       886

Qy    136  IleGlySerIleArgGlyLeuGluAspAlaIleArgThrGlnArgAspMetGluAsn       155
                  |||||||:::::          ||||||||
Db    887  TTTCAGCAGCGTCTGGAGAGACCAGAGCTGGAGCTCAGACGACCATTCGCCCAGAAAAAGC    946

Qy    156  ThrAspProSerGluGlnIleAlaAlaLysAlaValMetAspLysPheGlnThrGlnIleLeu  175
               :::|||||          :::|||||
Db    947  GAAAATCTGGAGCCCTGGAGTCCTCCAGGACAGC---AGCACCAGCTATACTGAAACCA      964

Qy    176  ProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPheMetProGlnMet           195
                                                        ||||||:::
Db    965  -----------------AAAGGTGACTCTGATGATGAGAAACCA--------------------  991

Qy    196  ArgLysAlaGlnAlaAlaAlaProSerValPheGlnGlnAlaLeuAlaLeuAlaArgAlaMet  215
               ||||||          ::::: |||
Db    992  AGCAGGCAAGAGCAAGACGATCATCTAGGGTC---AGACAGGCAAGAGCAGCTAAACTGTCT  1048

Qy    216  LeuGlyLysAsnAlaProValAlaGlyGlyArgGly-GluGlu------GlnArgMetMe    233
               |||                                 ::::: ::
Db   1049  GAGGGC--AGCCAACCTGCTGA-GGAGGAAGGAGGATCAAGAAACAACCTTCCAGAAACCT  1104
```

RESULT 9
US-09-949-016-5054
; Sequence 5054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

RESULT 10
US-09-917-254-40
; Sequence 40, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 40
; LENGTH: 5574
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-917-254-40

Alignment Scores:
Pred. No.:
Score:                          9.74e-06          Length:          5574
                                159.00            Matches:         137
Percent Similarity:             39.2%             Conservative:    121
Best Local Similarity:          20.8%             Mismatches:      212
Query Match:                    4.8%              Indels:          192
DB:                             3                 Gaps:            32

US-10-736-868-2 (1-643) x US-09-917-254-40 (1-5574)

Left column alignment:

```
Qy    82  GluValLeuGluLysValHisProAspGln--------FheAspLysTyrLysLeu 98
              |||     |||     :::::                  ::: ||||||||
Db  3859  GAGAACCTCACCCAGCAGTACGAGGAGGCGGCCGCTTATGATAAACTGAAAAGACC 3918

Qy    99  Lys----------------ValAspAspLeuAlaAlaAspAlaValMetGlnAla 112
             |||               :::|||||||||||    ||||||||
Db  3919  AAGAACAGGCTTCAGCAGGAGCTGGACGCGACCTGGTTGTTGATTTCGACAACCAGCGCAA 3978

Qy   113  GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
             ::::::|||||||     |||:::       |||
Db  3979  CTTCGTGTCCAACCTGGAAAAGAAGCAGCAGAGGAAA-------TTTGATCAGTTGTTAGCCGAG 4032

Qy   133  GlyIleProIleGlySerSer----------------------------- 139
             |||||||
Db  4033  GAGAAAAACATCTCTTCCAAATACGGGATGAGAGGACAGAGCTGAGCAGG 4092

Qy   140  --------IleArgGlyLeuGluAspAlaIleAlaArgThrGln 150
                :::::  |||    |||:::||
Db  4093  GAGAAGGAAACCAAGGCCCTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGGAAGCCAAA 4152

Qy   151  ArgAspMetGluAsnThrAspProSerGluGlnIleLeuAlaLysAlaValMetAspLysPhe 170
             :::::::|||||||     |||||||::::::|||
Db  4153  GAGGAACTCGAGGGACCAAC------AAAATGCTCAAAGCCGAAATGGAA------ 4197

Qy   171  GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
                                   :::::::|||
Db  4198  ---------------------GACCTGGTCAGCTCCAAGGATGACGTGGGC 4227

Qy   190  LysMetProGlnGlnMetArgLysGlyAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
             :::::::|||||||     |||    :::::
Db  4228  AAGAACGTCCATGAGCTGGAGAGTCCAAGCGGGCCCCAGATGCCAGATGGAGGAGATG 4287

Qy   210  LeuAlaGlnAsnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyTyrArgGlyGluGlu 229
             |||    |||:::|||
Db  4288  AAGGACCAGCTGGAAGAGCTGGAAGAGCTGCAAGCCACG------GAGGAC 4335

Qy   230  GlnArgMetMetAsnArgValAspGlnArgMetGln------------Gln 243
             :::::::|||||||
Db  4336  GCCAAACTG--------CGGCTGGAGTCAACATGCAGGGCGCTCAAGGCCAGTTCGAA 4386

Qy   244  ArgGluLeuGlnGluGluGlnAspGluAspGluAspGluAsnAspAspAspProSerValProArg 263
             |||||||     |||:::    |||
Db  4387  AGGGATCTCCAAGCCCGGACGAGCGACAGAATGAG------GAGAAGAGGAGGCAACTGCGAG 4440

Qy   264  ArgArgSerArgAspArgGlyGlnSerArgGluGluAlaGlyGluHisGlnAsnArgArgAspGluLeuAla 283
             ::::::|||||||     |||||||||||
Db  4441  AGACAGCTCACGAGTGATGAGACGGAAACAACGTGCCCTGGCA 4500

Qy   284  ArgArgLeuLysSerSerProArgLeuLysLeuGluLeuGlnAsnAlaGlnAlaGluValGlnSer 303
             :::|||||||     :::||||||
Db  4501  GCTGCGCAAAGAAG------AAGCTGGAAGGGAGGGGACCTGGAAGCGCTTCAGGCC 4554

Qy   304  LeuLeuSerTyrArgMetArgAspSerProLeuSerLysSerArgProLeu------- 321
             |||||||     :::
Db  4555  --GACTCTGCCATCAAGGGGGAGGGGGAGGAAGAGGCCATCAAGCCAGCTACGCAAACTGCAGGCT 4611

Qy   322  AlaMetAsnAsp---------------GluAspGluSerAlaPheArg---AlaMetGlu 335
             |||||||     :::
Db  4612  CAGATGAAGGACTTTCAAAGAGAGTTGGAAGATGCCGTGCCTGCCTCCAGAGATGAGATCTTT 4671

Qy   336  AlaArgAlaLysAspLeuAspAspSerGlnLeuValLeuGlyLeuHisGlyLeuPheGlyGlu 355
             ::::::|||||||     |||
Db  4672  GCCCAGAACGCCAAAGAACGAGGAAGAGAAAGACCAAGAGCTTG------GAA 4713

Qy   356  SerAspAspAspGluAspGluAspGluAsnLeuIleLeuAspProSerGluSerSerPhe 375
             :::  |||:::     |||:::
Db  4714  GCAAGAGACCTCATGCAGCTACAAGAGGAC------CTCGCCGCCGCCTGAGAGGGCTCGC 4764

Qy   376  ArgArgAlaProLeu---------ArgLeuSerSerGlyPheValGluLysLeuLysSer 392
             :::::::|||||||
Db  4765  AAACAAGCGGACCTCGAGAGGAGAGAACTGGCCAGTAGCCTGTCGGGA 4824
```

Right column alignment:

```
Qy   393  AsnAspGluLeuLysSerAlaLeuAspAspArgIleLeuGluLysTyrArgValAspAspValGluGlyLys 412
             ::: |||    ::::::  |||||||
Db  4825  AGGAACGCACTCCAGGACGAGAAGCCGCCTGGACCCCGATCGCCCAGCTGGAGGAG 4884

Qy   413  TyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyr-PheAlaPro 432
             |||:::       :::  ||||||||||||
Db  4885  GAGCTGGAGGAGGAGCAGGG-CAACATGGAGCCCATGAGCCGACCGGGTCC-GCAAAGCCA 4942

Qy   433  ArgLysIleProThr---------------------------ArgProArgLys 441
             ||||||     ||||||
Db  4943  CACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCCGCAGCACGGCCCAGAAGA 5002

Qy   442  Met----LeuProLeuLeuIleGlySerAspProLysValGlnGluLeuIleArgArgHis 460
             |||       :::
Db  5003  ATGAGAGTGCCC---------GGCCAGCTGCAGGTCCGAGCCGAGAACAACGAGCTCCGGAGCA 5053

Qy   461  ProSerThrGluTrpProIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn 480
                ::::::|||  :::|||||
Db  5054  AGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC--------------AAGTTCAAG 5094

Qy   481  ProSerLeuAlaAlaLeu-----------PheMetAspLysGluLeuGluAsnThr 495
             :::::::||||||||
Db  5095  TCCACCATGCGCGGCCTGGAGGCCAAGATTGCACAGTGCTGGAGCAGGTCGAGCAGGAG 5154

Qy   496  LeuLysGlyArgGlnMetLeuThr----------------------------- 503
             :::::::|||
Db  5155  GCCAGAGAAACAGGCGGCCACCAAGTCGCTGAAGCAGAGAAAGACAAGAAGTGAAGGAA 5214

Qy   504  -------------------------AspGlu 506
                                       :::|||
Db  5215  ATCTTCTGCAGGTGAGGACGGCGCCAAGATGGCCCAAGATGGCAGTACAACAAGGAGCAGCAGAG 5274

Qy   507  LysGlyArgThrArgValLysThrIleArgThrLeuArgProArgLeuPheGlyAlaProThr 526
             ||||||
Db  5275  AAAGGCAATGCCAGGTCAGGTCAGCAGCTCAAG------AGGCAGCTGGAGGAGGCAGCAGAG 5325

Qy   527  AlaLysAlaGluMetIleAspAla------------LysValPheGlnIleGluGlu 542
             |||||||     ::::::|||
Db  5326  GAGGAGTCCCAGCCATCAACGCCACCGGACGAGCTCGCAGCCGGAGCTGCAGGCTCGGATGAG 5382
```

Alignment Scores:

| | | |
|---|---|---|
| Pred. No.: | 1.35e-05 | |
| Score: | 159.00 | Length: 6861 |
| Percent Similarity: | 39.2% | Matches: 137 |
| Best Local Similarity: | 20.8% | Conservative: 121 |
| Query Match: | 4.8% | Mismatches: 212 |
| DB: | | Indels: 192 |
| | | Gaps: 32 |

US-10-736-868-2 (1-643) x US-09-949-016-1240 (1-6861)

```
Qy     15  IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer     34
               :::|||   |||||||||::::||          :::
Db   4016  GTGGCGTCCCTCAGTTCCCAGTCCCAGGACACCCAGGAGCTG------------------   4057

Qy     35  SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu     54
               :::|||    ||||||||||       :::     |||||
Db   4058  ---CTTCAAGAGAGAAACCCGGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG   4114

Qy     54                                                              54
Db   4115  GAGGAGGCGGAACAGCCTGCCAAGACCAGCTGGACGAGGAGATGGAGGCCAAGCAGAACCTG   4174

Qy     55  ------------LeuMetGlyValGlnPheValAspAlaLeuIleLysGlyGlyGln     69
                            :::  |||||||  |||::|        :::
Db   4175  GAGCGGCCACATCTCCACTCTCCAACATCCAGCTCTCCGACTCGAAG---AAGAGCTGCAG   4231

Qy     70  ------------MetGluMetAlaLysMetGlyAlaPheLysThrGlnLeu     81
                            |||                :::  :::::
Db   4232  GACTTTGCCAGCACCGTGGAAGCTCTCGAAGACGAAGAGAGATC-----AAGGAGATC   4291

Qy     82  GluValLeuGluLysValHisProAspGln-----------PheAspLysTyrLysLysLeu     98
               |||       ||| :::                        :::
Db   4292  GAGAACCTCACCCAGCAGTACCGAGGAAGGCGGCCCCTTATGATAAACTGAAAAGACC   4351

Qy     99  Lys------------ValAspAspLeuAlaLeuAlaAspAlaValMetGlnAsnAla    112
               |||                |||||||||:::::
Db   4352  AAGAACAGGCTTCAGCAGACGGAGCTGGACGACCTGGTTGTTGATTTGGACAACCAGCGGCAA   4411

Qy    113  GluMetAlaLysLeuGlnLeuProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn    132
               :::::: ||||||          |||
Db   4412  CTCGTGTCCAACCTGGAAAAGACAGCAGAAA------TTTGATCAGTTGTTAGCCGAG   4465

Qy    133  GlyIleProLeuGlySerSer--------------------    139
               |||
Db   4466  GAGAAAAACATCTCTTCCAAATACGCCGATGAGAGGACAGAGCTGAGGCAGCAGCCAGG   4525

Qy    140  ------------IleArgGlyLeuGluAspAlaIleAlaIleArgThrGln    150
                            |||||||||   :::::
Db   4526  GAGAAGGAAACCAAGGACCCTGTGTCCCTGGCTCGGGCCCTTGAAGAGGCCTTGAAGCCAAA   4585

Qy    151  ArgAspMetGluAsnThrAspProSerGluGlnAsnIleAlaLysAlaValMetAspLysPhe    170
               :::::::|||:::      ||||| |||:::
Db   4586  GAGGAACTCGAGCGCGACCAAC------AAAATGCTCAAAGCCCGAAATGGAA-----   4630

Qy    171  GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLeuLysAsnProPhe---    189
               :::                   |||::: |||:::
Db   4631  ------------GACCTGGTCAGCTCCAAGGATGACGTGGGGC   4660

Qy    190  LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla    209
               |||            :::::   ||||||
Db   4661  AAGAAGACGTCCATGAGCTGGAGAAGCTCCAAGCGGCCCCTGGAGATGGAGGAGATG   4720

Qy    210  LeuAlaGlnAsnArgAlaMetLeuGlyLysLysAsnAlaProValAlaGlyLyArgGlyGluGlu    229
               |||                            |||:::
Db   4721  AAGAGCCAGCTGGAGACGCTGGAGGAGCTGCCAAGCCACG------------GAGGAC   4768

Qy    230  GlnArgMetMetAsnArgValAspGlyHisArgMetGln-----------------Gln    243
               |||                                          :::
Db   4769  GCCAAACTG--------CGGCTGGAGTCAACATGCAGGGCCGCCTCAAGGGCCAGTTCGAA   4819

Qy    244  ArgGluGluGlnGluGluAspGluAspGluAspAspLeuGluAspGluAspValProValPheArg    263
               |||||||:::         :::        ||| |||
Db   4820  AGGGGATCTCCAAGCCCGGGACCAGACAGAATGAG------GAGAAGAGGAGGCAACTGCAG   4873

Qy    264  ArgArgSerSerAspGlyGluProGlnSerGluGlnLeuAlaGluHisArgArgAspAspLeuAla    283
               |||::::          :::     |||::::
Db   4874  AGACAGCTTCACGAGTATGAGACGAACGTGGAAGACGAGAACAAGCAACGTGCCCTGGCA   4933

Qy    284  ArgArgLeuLysSerSerProArgLeuLysGluLeuGlnLeuAsnAlaGluGluValGlnLnSer    303
               |||::::::                                        :::::
Db   4934  GCTGCAGCAAAGAAG-----AAGCTGGAAGGGACCTGAAAGACCTTGGAGCTTCAGGCC   4987
```

```
Qy    304  LeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu-------    321
               :::|||||          :::       |||
Db   4988  ---GACTCTGCCATCAAGGGGGACGGGGAGGAGGAAGCCATCAAGCAGCTACGCGAAACTGCAGGCT   5044

Qy    322  AlaMetAsnAsp-------------------GluAspGluSerAlaPheArg--AlaMetGlu    335
               |||                                  |||           :::
Db   5045  CAGATGAAGGACTTTCAAAGAGAGCTCAAGAGAGCCCGTGCCTCCAGAGATGAGATCTTT   5104

Qy    336  AlaArgAlaLysLeuAspGlnLysLysSerGlnLeuValLeuGlyLeuHisGlyPheGlyGlu    355
               ||||||||||||                   |||
Db   5105  GCCACAGCCAAAGAAGAATGAGAGAAAAGCCAAGAGCTTG-------------GAA   5146

Qy    356  SerAspAspAspAlaGluGlyAspGluAspGluAsnLeuIleAspProSerGlnAsnSerPhe    375
               :::::                          |||||||||:::
Db   5147  GCAGACCTCATGCAGCTACAAGAGGAC--------CTCGCCGCCGTGAGCAGGGGCTCGC   5197

Qy    376  ArgArgAlaProLeu------------ArgLeuSerGlyPheValGluLysGluLeuLysSer    392
               |||                         :::|||||||
Db   5198  AAACAAGGCGACCTCGAGACAGGAGGAACTGGCAGAGGAGCTGCCAGTAGCCTGTCGGGA   5257

Qy    393  AsnAspGluLeuLysSerAlaAlaAspArgArgIleLysTyrArgValAspAspValGluLys    412
               ||||||     :::                  ||||| :::::
Db   5258  AGGAACGGACCTCAGGACGCAGAGAGGCGCCCTGGAGGCCGATGCCCCAGCTGGAGGAG   5317

Qy    413  TyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaPro    432
               |||        ||| :::                       |||
Db   5318  GAGCTGGAGGAGGAGCAGCAGG--CAACATCGAGGCCATGAGCGACCTGGAGTCC--GCAAAGCCA   5375

Qy    433  ArgLysIleProThr-------------------ArgProArgLys    441
               |||                             ||||||||||
Db   5376  CACAGCAGGCCGAGCAGCTCAGCCAACGAGCTGCCACAGAGCCGGCAGCACGGCCCAGAGA   5435

Qy    442  Met---LeuProLeuLeuIleGlySerAspAspProLysValGlnIleGluIleArgArgHis    460
               |||      ||||||                        ::: 
Db   5436  ATGAGAGTGCCC------------GGCAGCAGCTCGAGCGGCAGAACAAGAGACTCCGAGCA   5486

Qy    461  ProSerThrGluTrpLysIleAlaLysGluSerArgValLeuThrAsnLeuLysAsnAsn    480
               |||                     |||:::
Db   5487  AGCTCCACGAGAATGGAGGGG-GCGGTCAAGTCC-----------------AAGTTCAAG   5527

Qy    481  ProSerLeuAlaAlaLeu-------------------PheMetAspLysLeuGluAsnThr    495
               |||                                  :::::|||||||
Db   5528  TCCACCATCGCCGGCGTCTGGAGGCCAAGATTGCACAGTCAGCAGGTCAGCGAGGAG   5587

Qy    496  LeuLysGlyArgGlnMetLeuThr-------------------    503
               |||
Db   5588  GCCAGAGAGAAACAGGCGCCACCAGTCGCTGAAGCAGAAAGACAAGAAGTCGAAGGAA   5647

Qy    504  ------------AspGlu---------------------Gln    506
                            :::                       |||
Db   5648  ATCTTGCTGCAGTGAGCGGGAGGACGAGCGCAAGATGGCCAAGGAGCAGCAGCAGAG   5707

Qy    507  LysGlyArgThrArgValLysThrIleArgAlaLeuProArgLeuPheGlyAlaProThr    526
               |||                     :::::
Db   5708  AAAGGCAATGCCAGGTCAAGCAGCTCAAG--------------AGGCAGCTGGAGGAGGCAGAG   5758

Qy    527  AlaLysAlaGluMetIleAspAla-----------LysValPheGlnAspIleGluGlu    542
               |||                              :::::::
Db   5759  GAGGAGTCCCAGCTGCAACATCAACGCCCAACCCAGAAGGGCCAGAAGTCGCAGCGGGAGCTGGATGAG   5815
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RESULT 12
US-09-949-016-1241
; Sequence 1241, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE:  2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

```
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 1241
;  LENGTH: 6861
;  TYPE: DNA
;  ORGANISM: Human
US-09-949-016-1241

Alignment Scores:
Pred. No.:
Score:                  1.35e-05        Length:         6861
                        159.00          Matches:        137
Percent Similarity:     39.2%           Conservative:   121
Best Local Similarity:  20.8%           Mismatches:     212
Query Match:            4.8%            Indels:         192
DB:                                     Gaps:           32

US-10-736-868-2 (1-643)  x  US-09-949-016-1241 (1-6861)
```

```
Qy    15  IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaProGlyAlaLeuLeuSer 34
          :::||   |||||   ||     ::      :::
Db  4016  GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGCTG--------------------- 4057

Qy    35  SerLeuValGlyLysSerHisGlnLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
          ||||||      :::::: |||||||            ::      |||||||
Db  4058  ---CTTCAAGAAGAAACCCGCAGAAGCTCAACGTGTCTACGAAGCTGCGCCAGCTGGAG 4114

Qy    54                                                          54
Db  4115  GAGGAGCGGAACAGCCTGCGAAGACCAGCTCGACGAGGAGATGGAGCGCCAAGCAGACCTG 4174

Qy    55  --------------LeuMetGlyValGlnPheValAlaAspAlaLeuLeuIleLeuLysLysGlyGln 69
                        ||      ||| |                  ||||||
Db  4175  GAGCGCCACATCTCCACTCTCCAACATCCAGCTCTCCGACTCGAAG----AAGAAGTGCAG 4231

Qy    70  ----------MetGluMetAlaLysMetGlyAlaLysPheLysThrGlnLeu 81
                    ||      :::                  ::      ::::::::
Db  4232  GACTTTGCCAGCACCGTGGAAGCTCTGGAAGAGGGGAAGAGAGGTTTCCAGAAGAGAGATC 4291

Qy    82  GluValLeuGluLysValHisProAspGln----------PheAspLysTyrLysLysLeu 98
          |||            ||| ::  ::::::::            :::|||
Db  4292  GAGAAGACCTCACCCAGCAGTACGAGGAGAAGAGGCGGCCGCCTTATGATAAACTGGAAAAGACC 4351

Qy    99  Lys------------------ValAspAspLeuAlaAlaAspArgAlaValMetGlnAlaValAlaAla 112
          |||                  :::|||
Db  4352  AAGAACAGGCTTCAGCGAGAGCTGGACGACGACGCTGGTTGTTGATTTGGACAACCAGCGGCAA 4411

Qy   113  GluMetAlaLysLeuGlnLysProLysSerGlyAspGlyAsnAlaPheIleLeuAspMetLeuAsnGlyAsn 132
          :::::::      |||||::|||:::   ||
Db  4412  CTCGTGTCCAACCTGAAAAGAAGACAGAGAAA------TTTGATCAGTTGTTAGCCGAG 4465

Qy   133  GlyIleProIleGlySerSer 139
          |||      ||
Db  4466  GAGAAAAACATCTCTTCCAAATACGGCGGATGAGAGGAGCAGAGAGCTGAGGCAGAAGCCAGG 4525

Qy   140  ----------------IleArgGlyLeuGluAspGlyAlaIleArgThrGln 150
                          :::::::|||||:::|||:::
Db  4526  GAGAGGGAAACCAAGGGCCCTGTCCCGGCCCTTGGAAGAGCCCTTGGAAGCCAAA 4585

Qy   151  ArgAspMetGluAsnThrAspProSerGluGlnIleLeuAlaLysAlaValMetAspLysPhe 170
          ||      ::::::||:::      :::::: |||||||
Db  4586  GAGGAACTCGAGCGCGGACCAAC---------AAAATGCTCAAAGCCAAAATGGAA------ 4630

Qy   171  GlnThrGlnIleLeuProGlyLeuValAlaGlyGlyLeuAlaAsnMetIleAlaGlyLysAsnProPhe--- 189
          |||||| ||      :::::: :::|||      :::::::
Db  4631  ---------GACCTGGTCAGCTCCAAGGATGACCTGGGC------------------- 4660

Qy   190  LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnAla 209
          |||          :::|||       :::       |||
Db  4648  ATCTTGCTCAGGTGGACGAGCTGGAGGAAGTCCAAGCGGCCAGAGTAGGAGGCAGCAGAG 5707
```

```
Db  4661  AAGAACGTCCATGAGCTGGAGAAGTCCAAGCGGCGGGCCCTGGAGACCCAGATGGAGGAGATG 4720
Qy   210  LeuAlaGlnArgAlaMetLeuGlyLysAsnAlaProValAlaGlyGlyArgGlyArgGlyGluGlu 229
Db  4721  AAGACGCAGCTGGAGAGGCTGGAGGACGAGCTGCAAGCCACG------------GAGGAC 4768
Qy   230  GlnArgMetMetAsnArgValAspGlnArgMetGln 243
          :::::::      |||||
Db  4769  GCCAAACTG------CGCTGGAAGTCAACATGCAGGGCCTCAGGGCCTCAGGGCCCAGTTCGAA 4819
Qy   244  ArgGluLeuGlnGluGlnLeuAspGluGlnAspAspArgLeuGluAspGluAspAspProValProArg 263
          ||||:::||:::|||        :::
Db  4820  AGGGATCTCCAAGCCCGGACAGCAGAATGAG------GAGAAGAGAGGCAACTGCAG 4873
Qy   264  ArgArgSerSerAspGlyGlnProGlnSerGluAlaGluHisGlnArgArgAspLeuAla 283
          :::||         ::       :::::::   :::|||
Db  4874  AGACAGCTTCACGAGTATGAGACGAGGAACTGAAGACGAGCGAAAGACAACGTGCCTGGCA 4933
Qy   284  ArgArgLeuLysSerSerProArgLeuLysGluLysLeuLeuGluLeuGluAsnAlaLeuGlnSer 303
          :::::::::::||      |||||
Db  4934  GCTGCAGCAAAGAAG------AAGCTGGAAGGGAGGGACCTGAAAGACCTTGGAGCTTCAGGCC 4987
Qy   304  LeuLeuSerTyrArgGlnArgMetArgAspSerProLeuSerLysArgArgProLeu------- 321
          :::||   ::::::|||         ::
Db  4988  ---GACTTCTGCCATCAAGGGAGGGGAGGAAGCCATCAAGCACTACGCCAAACTGCAGGCT 5044
Qy   322  AlaMetAsnAsp---------GluAspGluSerAlaPheArg---AlaMetGlu 335
          ||||                  ||                ::::::
Db  5045  CAGATGAAGGACTTTCAAGAGAGCCTGGAAGAGGGGAACTGGGGAATGGAGAGATCTTT 5104
Qy   336  AlaArgAlaLysLeuAspLysGlnLeuValLeuSerGlnLeuHisGlyGluLeuHisGlyPheGlyGlu 355
          :::      ||::||:::         ||
Db  5105  GCCAACAGCCAAAGAAGATGAGAAGGGAAAGCCAAGAGCTG------------GAA 5146
Qy   356  SerAspAspGluGlyGluGluAspGluGluGluAsnLeuIleLeuAspProSerGluAsnSerPhe 375
          :::|||         :::::::|||
Db  5147  GCAGACCCTCATGCAGCTACAAGAGGAC------------CTCCGCCGCCTGAGAGGGCTCGC 5197
Qy   376  ArgArgAlaProLeu--------ArgLeuSerSerGlyPheValGluLysLysLeuLysSer 392
          :::|||||         ::      :::::::
Db  5198  AAACAAGCGGACCTCGAGAAGGAGGAGAACTGGCAGAAGGAGATTGTTCGGGA 5257
Qy   393  AsnAspAspLysSerAlaLeuAlaLeuAspProLysArgIleLeuLysTyrArgGlyValGluValLys 412
          :::      |||:::      |||||||
Db  5258  AGGGAACGCACTCCAGGACGAGGAAGCGCCGCCCGATCGCCCAGCTGGACGAG 5317
Qy   413  TyrLeuAlaProLysProMetGluProMetProLysProGlnPheAsnProGlnProTyrPheAlaPro 432
          :::|||   :::::       ::::::|||
Db  5318  GAGCTGGAGGAGGAGCAGGG-CAACATGGAGGCCATGAGCACCGGGGTCC--GCAAAGCCA 5375
Qy   433  ----------------------------------ArgProArgLys 441
                                            |||
Db  5376  CACAGCAGGCCCGAGCAGCTCCAGCAACGAGCTGGCCACAGAGCGCGCACGGCCGAGAGA 5435
Qy   442  Met---LeuProLeuLeuIleGlySerAspProLysValGlnIleGluIleArgArgHis 460
          |||         :::::::|||
Db  5436  ATGAGAGTGCCC-----------GGCAGCAGTCGCAGAACAAGGAGCTCCGGAGCA 5486
Qy   461  ProSerThrGluTrpProIleLeuAlaLysGluLeuThrArgAsnLeuLysAsnAsn 480
          |||||      :::::::||||||
Db  5487  AGCTCCACGAGCGGATGGAGGGG-GCCGTCAAGTCC 5527
Qy   481  ProSerLeuAlaAlaLeu-----------PheMetAspLysLeuAsnThr 495
          |||||||      :::::::
Db  5528  TCCACCATGCGCGGCCTGGAGGCCAAGATTGCACAGCTGGAGGAGCAGCAGGAG 5587
Qy   496  LeuLysLysGlyArgGlnMetLeuThr-------------- 503
          |||||
Db  5588  GCCAGAGAGAAACAGGCGGCCACCAACAGCCTGTGAAGCAGGAGAAAGACAAGAAGCTGAAGGAA 5647
Qy   504  ------------------AspGlu------------------GlnGln 506
                            ||||||                  :::
Db  5648  ATCTTGCTCAGGTGGACGAGCTGGAGGAAGTCCAAGCGGCCAGAGTAGGAGGCAGCAGAG 5707
```

Qy    507  LysGlyArgThrArgValLysThrIleAlaArgLysProArgLeuPheGlyAlaProThr  526
                |||||   :||||      |:||||        ::|||:
Db   5708  AAAGGCAATGCCAGGTCAAGCAGCTCAAG---------AGGCAGCTGGAGGAGGCAGAG  5758

Qy    527  AlaLysAlaGluMetIleAspAla----------LysValPheGlnAspIleGluGlu  542
               :::::|:|||          |||:         |||::  ::::|:::||||
Db   5759  GAGGAGTCCCAGCCGCATCAACGCCACCCAGGAGAGCTGCGGGGAGCTGGATGAG  5815

RESULT 13
US-09-949-016-1242
; Sequence 1242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1242
; LENGTH: 6861
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1242

Alignment Scores:
Pred. No.:                   1.35e-05      Length:          6861
Score:                       159.00        Matches:          137
Percent Similarity:          39.2%         Conservative:     121
Best Local Similarity:       20.8%         Mismatches:       212
Query Match:                 4.8%          Indels:           192
DB:                          3             Gaps:              32

US-10-736-868-2 (1-643) x US-09-949-016-1242 (1-6861)

Qy     15  IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaLeuLeuSer  34
               ::|||   |||||||   ::|||||:|||:      ||  :::
Db   4016  GTGGCGTCCCTCAGTTCCCAGCTCCAGGACACCCAGGAGCTG---------  4057

Qy     35  SerLeuValGlyLysSerHisGlnLysHisGlnLeuProLeuAlaProSerMetGluAlaLeuGlu  54
               |||   :::::  ||||||||         :::    :::
Db   4058  ---CTTCAAGAAGAAACCCGGCAGAGCTCAACGTGCTCTACGAAGCTGCGCGCCAGCTGGAG  4114

Qy     54                                                                   54
                                                                       |||
Db   4115  GAGGAGCGGGAACAGCCTGCAAGCCAGCTGGACGAGGAGATGGAGGCCAAGCAGAGACCTG  4174

Qy     55  ----------LeuMetGlyValGlnPheValAspGlnPheAlaLeuLeuLeuLysGlyGln  69
                      :::||||||||      :::|||||||||||    |||||
Db   4175  GAGCGCCACCATCTCCAACATCCAGCTCTCCAGCTCGAAG---AAGAAGCTGCAG  4231

Qy     70  ----------------MetGluMetAlaLysGlyGlyGluAlaGlyAspGlyArgArgLys  81
                           :|||    |||   |||||   ::::|||    ::::::
Db   4232  GACTTTGCCACCGTGGAGGAGCTGGAGGAGGGGAAGAAGAGAGAGGTTCCAGAAGGAGATC  4291

Qy     82  GluValLeuGluLysValHisProAspGln----------PheAspLysTyrLysLysLeu  98
               |:||   |||     :::     :::          |||||||   :::||||||
Db   4292  GAGAACCTCACCGAGAGGAAGGCGGCCGCCTTATGATAAACTGAAAAAGACC  4351

Qy     99  Lys-------------------ValAspAspLeuAlaAlaAspAlaValMetGlnGlnAla  112
               |||                 ::::||||||   :::     :::
Db   4352  AAGAACAGGCTTCAGCAGGAGCTTGGACGACCTGGTTGTTGATTTGGACAACCAGCGCAA  4411

Qy    113  GluMetAlaLysLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAspAspGlyAsn  132
               ||||||||||   ::::   :::
Db   4412  CTCGTGTCCAACCTGGAAAAGAGCAGGAAA-------TTTGATCAGTCAGTTGTTAGCCGAG  4465

Qy    133  GlyIleProIleGlySer---------------------------------------------  139
               |||   |||
Db   4466  GAGAAAAACATCTCTTCCAAATACGCCGGTGAGGACGAGAGCTGAGGCAGCAGAAGCCAGG  4525

Qy    140  -------------------------------------IleArgGlyLeuGluAspAlaIleArgThrGln  150
                                                    |||   ::||||||||      :::||||
Db   4526  GAGGAGGAAACCAAGGCCCTGTCCCTGGCTCGGCCCTTGAAGAGCCTTGGAAGCCAAA  4585

Qy    151  ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe  170
               :::|||   |||||||   :::||:       :::|||||
Db   4586  GAGGAACTCGAGCGACCAAC---------AAAATGCTCAAGCGCAAATGAA-------  4630

Qy    171  GlnThrGlnIleLeuProGlyLeuValAlaAsnMetIleAlaGlyLeuAsnProPhe---  189
                                                        ||:::
Db   4631  ---------GACCTGGTCAGCTCCAAGGATGACGTGGGC  4660

Qy    190  LysMetProGlnGlnMetArgLysAlaGlnAlaAlaProSerSerValPheGlnGlnGlnAla  209
               |||      |||||||      ::|||||      :::
Db   4661  AAGAAACGTCCATGAGCTGGAAGTCCAAGCGGCCCTGGAGACCCAGATGGAGGAGATG  4720

Qy    210  LeuAlaAlaMetLeuGlyLysLysAsnAlaProValAlaGlyLeuGlyArgGlyGluGlu  229
               ||:::     |||||||||            :::|||
Db   4721  AAGACGGACTGGAAGACTGGAGGACGAGCTGCAAGCCACG-----------------  4768

Qy    230  GlnArgMetMetAsnArgValAspAspGlnArgMetGln----------------------Gln  243
                                           :::
Db   4769  GCCAAACTG------------CGGCTGGAGTCAACATGCAGGAGACTCAAGGGCCAGTTCGAA  4819

Qy    244  ArgGluLeuGlnGluGluAspGluAspLeuGluAspAspLeuGluAspAspLeuGluAspValProArg  263
               :::                                               |||
Db   4820  AGGGATCTTCCAAGCCCCGGACGACAGAGAATGAG------GAGAAGAGGAGGCCAACTGCAG  4873

Qy    264  ArgArgSerSerAspGlyProGlnSerGlyGlnAlaGluHisArgArgGlnArgLeuAla  283
               :|||   ||| ::::::           ::::||||
Db   4874  AGACAGCTTCACGAGTATGAGACGAACTGAAGAGCGAAGACAACGTGCCCTGGCA  4933

Qy    284  ArgArgLeuLysSerSerProArgLeuLysGluLeuGlnAsnAlaGluValGlnSer  303
                                :::|||||||            |||:::
Db   4934  GCTGCAGCAAAGAAG------AAGCTGGAAGGGGGAACCTGAAAGACCTGGAGCTTCAGGCC  4987

Qy    304  LeuLeuSerTyrGlnArgMetArgAspSerProLeuSerLysArgArgProLeu---------  321
               |||||||      :::
Db   4988  ---GACTCTGCCATCAAGGGAGCTGGAGGAGGAGCCATCAAGCAGCTACGCAAACTGCAGGCT  5044

Qy    322  AlaMetAsnAsp-------------------------GluAspGluSerAlaPheArg---AlaMetGlu  335
               :::|||||||                         |||
Db   5045  CAGATGAAGGACTTTCAAAGAGGAGCTGGAAGATGCCCGTGCCTTCCAGAGATGAGATCTTT  5104

Qy    336  AlaArgLeuLysSerProAlaLysLysAspAlaArgIleLysTyrArgValAspLysValGlyLys  355
               :::|||||||      ::|||||   :::   |||
Db   5105  GCCACAGCCAAAGAAGAATGAGAGAAGAAAGCCAAGAGCTTG----------GAA  5146

Qy    356  SerAspAspAlaGlyLysAspGluAspGluIleLeuAspGluAsnSerPhe  375
               :::|||||||   :::|||||||      :::
Db   5147  GCAGACCTCATGCAGCTACAAGAGGAC-----------------CTCGCCCCGCTGAGAGGGCTCGC  5197

Qy    376  ArgArgAlaProLeu--------------ArgLeuSerGlyPheValGluLysGluLysLysSer  392
               :::||||||         |:::
Db   5198  AACAAGCCGACCTCGAGAAGGAGGAACTGCCAGAGGAGCTGGCCAGTAGCCTGTCGGA  5257

Qy    393  AsnAspGluLeuLysSerAlaLeuAspAspArgIleLysTyrArgValAspAspValLys  412
               :::   ||||||   |||      :::||||||
Db   5258  AGGAAACCACTCCAGGACGAGGCGGCCCGCTGGAGGCCCAGCTGGAGGAG  5317

Qy    413  TyrLeuAlaProLysProMetGluPheAsnProLysProGlyTyrPheAlaPro  432
               :::||||||||   ::::::
Db   5318  GAGCTGGAGGAGGAGCAGGG--CAACATGAGGGCCATGAGCGACCGGGGTCC-GCAAAGCCA  5375

Qy    433  ArgProArgLys---------------------------------------------------  441
               :||||||||||
Db             ArgLysIleProThr----------
                       ||||||   :::

```
Db    5376 CACAGCAGGCCGAGCAGCTCAGCAACGAGCTGGCCACAGAGCGCAGCACGGCCCAGAAGA 5435

Qy      82 GluValLeuGluLysValHisProAspGlnPheAspLysTyrLysLeuLysValAsp 101
               |||:::::
Db   12710 GAA-------GAGCGGTACGACCTGCCCGCCGATCACCCCTCAAGGCCCTCCTT 12657

Qy     442 Met---LeuProLeuLeuIleGlySerAspProLysValGlnGluGluIleArgArgHis 460
               |||  ::|||||                                     :::
Db    5436 ATGAGAGTGCCC------GGCAGCAGCTCGAGCGCGGCAGAACAAGGAGCTCCGGAGCA 5486

Qy     102 AspLeuAlaAlaAspAlaValMetGlnGlnAlaGlyLeuMetAlaLysLeuGln 118
               ::: |||||||||
Db   12656 GAGACGGTTGGAGTCGCCGCCCTGAGCAACGAACAGTCCCTCTGAACGCAATGGAG 12597

Qy     461 ProSerThrGluTrpLysIleAlaLysGlySerArgValLeuThrAsnLeuLysAsnAsn 480
               ||||||  |||| :::|||  :::|||
Db    5487 AGCTCCACGAGATGGAGGGG-GCCGTCAAGTCC------------AAGTTCAAG 5527

Qy     119 ----------------------ProLysSerGlyAsnAlaPheIleAspMetLeuAsn 130
                                     ||||:::|||
Db   12596 GGGGCCTACCGCCAGTTCTTCACGCCCAAGACGGGAAAG-------CTCGTCACC 12549

Qy     481 ProSerLeuAlaLeu----------------PheMetAspAspLysLeuGluAsnThr 495
               ||||||                         :::|||||||||
Db    5528 TCCACCATCCGGCGCGTCGGAGGCCAAGATTGCACAGCTGGAGGAGCAGGTCGAGCAGGAG 5587

Qy     496 LeuLysGlyArgGlnMetLeuThr---------IleGlySerIleArgGlyLeu---GluAspAlaIleArg 148
               :::  ||||:::|||                   ||||||:::|||
Db    5588 GCCAGAGAAACAGGCGGCGCCACCAAGTCGCTGAAGCAGCAGAAAGCAAGAGCTGAAGGAA 5647

Qy     149 ---ThrGlnArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMet 167
                  |||
Db   12488 TTGACTCAGCGGTTGGCGGAG-------------ATCGAGCAGCTTGCCAGCGAGAGCATG 12441

Qy     504 ----------------AspGlu------------------------Gln 506
                                |||||                        :::
Db    5648 ATCTTGTCGCAGGTGGAGGACGGCCAAGATGCCGAGCAGTACAAGGAGCAGGCAGAG 5707

Qy     168 AspLysPheGlnThrGlnIleLeuProGlyLeuValAlaAlaAsnMetIleAlaGlyLysLysAsn 187
               |||  :::|||  :::||| :::
Db   12440 GACCTCCGGCCAGAAGCAGCTC------------------------------------------- 12420

Qy     507 LysGlyArgThrIleArgAlaLeuProArgLeuPheGlyAlaProThr 526
               :::  |||                        :::||| :::
Db    5708 AAAGGCAATGCCAGGGTCAAGCAGCTCAAG--------AGGCAGCTGAGGAGGCAGCAGAG 5758

Qy     188 ProPheLysMetProGlnMetArgLysAlaAlaGlnAlaAlaAlaAlaProSerValPheGln 207
                  ::::::                 ::::::
Db   12419 -----TCCCTGGCGGAGGAACGGCAGGACCTATGCAGCGCGCTCGCTAGCTG---CAG 12369

Qy     527 AlaLysAlaGluMetIleAspAla--------LysValPheGlnAspIleGluGlu 542
               ::::::                       ||| ::::::         |||
Db    5759 GAGGAGTCCCAGCGCCATCAACGCCAACCCACAGGAAGCTCGAGCGGGAGCTGGATGAG 5815

Qy     208 GlnAlaLeuAlaGlnArgAlaMetLeuAlaLysAsnAlaAsnAlaProValAlaGlyValGlyArgGly 227
               :::  ::::|||||||
Db   12368 GAGCGCCATCGCGAGGAGGAGAAGCTGGAGCCGCGGCTCCGGGAAGGAGACGTC 12309

Qy     228 GluGlnGlnArgMetMetMetAsnArgValAspGlnArg 241
               |||                              ::: Met
Db   12308 GAGGCTCAGCGAAAAGAGTGGCAGGCGCTGACCAGCACGGAGCAGAGCTTCTCGCGCTC 12249

Qy     242 GlnGlnArgGluLeuGlnGlnGluAsp--------GluAspAspAspLeuGluGluAsp 258
               :::|||                        |||  :::|||
Db   12248 CAGCAGAAGGTGGTCCAGGACCTGTCTGGCTCGCAACGAGCCGGCCTTGCAGGAG 12189

Qy     259 GluAspValProArgArgArgSerSerAspGlyGluProGlnSerGluAlaGluHisGln 278
               |||                              |||
Db   12188 GCCCAGGACTCGTCCGGCGCGCGCCGAAGACGGGGTCGCGAAGCACGGAGCGACACAAG 12129

Qy     279 ArgArgAspLeuAlaArgArgLeuLysSerProArgLeuLysGluLeuGlnAsn 298
                                                                ||||||
Db   12128 -----------------------------------------GCTCAGCAG 12120

Qy     299 AlaGluAlaValGlnSerLeuLeuSerTyrGlnArgMetArgAspProLeuSerLysArg 318
               |||:::||| ::::::                              |||||| :::
Db   12119 GGGGAGGTGGAG------CTGCGGAGCAGCCGGTGAACGAGGACGACTCCTCGAA--- 12069

Qy     319 ArgProLeuAlaMetAsnAspGluSerAlaPheAlaMetGluAlaArgAla 338
               :::||||||                            :::||||||||||
Db   12068 ----------------------------------GATGCGCGGCGCT 12057

Qy     339 LysLeuAspGlnLysSerGlnLeuValLeuHisGlyPheGlyGluSerAspAsp 358
               :::                                ::::::
Db   12056 TCCCTGGCGGAGCAGCGGAAGTTG------------------------------- 12033

Qy     359 AspGluGluAspGluAspGluAsnLeuIleAspProSerGluAsnSerPheArgArgAla 378
               :::                     :::                     :::
Db   12032 GACGGGCTCGTCAAGCAGGAGACGCCAGTGGAGATGCCGAGGAATGCCCGACGCAAG 11973

Qy     379 ProLeuArgLeuSerSerGlyProPheValGluLeuLysSerAsnAspGlu--------- 395
               :::
Db   11972 ACTGCGGCGCGCTTCAAGACGCCTTCCAGACGCGCGAGGTAAAGCGCCGCCGAGGAGGTGCAGCGC 11913

Qy     396 ---LeuLysSerAlaLeuAspArgIleLysTyrArgValAspAspValGluLysTyrLeu 414
                  :::||||||||||||                          :::|||
Db   11912 AAGCTGAATCAGGCCCCTGGACAGGGCTTGGCTGCTTGTTGGTTGAATCAGTCG---TCCTTCACT 11856
```

RESULT 14
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US-09-902-540-1175/c
; Sequence 1175, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1175
; LENGTH: 19269
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1175

Alignment Scores:
Pred. No.:                                Length:        19269
Score:             7.73e-05               Matches:       125
                   158.50                 Conservative:  106
Percent Similarity: 37.3%                 Mismatches:    215
Best Local Similarity: 20.2%              Indels:        173
Query Match:       4.8%                   Gaps:          29
DB:                3

US-10-736-868-2 (1-643)  x  US-09-902-540-1175 (1-19269)
```

```
Qy      27 AspAlaProGlyAlaLeuSerSerLeuValGlyLysSerHisGlnLysLeuProLeu 46
               ::|||||||                                   :::
Db   12884 GACGACGCCAGTAGCGTCCTGATGAGTGGACGGGAGTCGGTTGGAGCCGG------CTC 12831

Qy      47 AlaProSerMetGluAlaLeuGluLeuMetGlyValGlnPheVal----------- 61
               |||||||||||
Db   12830 GCTGAATCGGAGGCCAGTGGCGTTGCCGTCTTCCTTGTCTTCCAGCGTGCCCGGC 12771

Qy      62 AspAlaLeuIleLysLysGlyGlnMetGluMetAlaLysGlyAlaPheLysThrGlnLeu 81
               ::: :::        |||:::|||||||          :::||| :::
Db   12770 AACGGCGTGACGAAGGTGGGCGAACTGGGCGTTGCGGTTGCTTGTTGAATCAGTCG 12711
```

```
Alignment Scores:
Pred. No.:              1.86e-05        Length:      6175
Score:                  157.00          Matches:     127
Percent Similarity:     38.3%           Conservative: 127
Best Local Similarity:  19.2%           Mismatches:  211
Query Match:            4.8%            Indels:      198
DB:                                      Gaps:        32

US-10-736-868-2 (1-643) x US-08-875-435B-1 (1-6175)

Qy     15 IleAlaProLeuSerAlaGlnSerProSerThrSerAspAlaProGlyAlaAlaLeuLeuSer 34
             :::   ||||   |||        :::        ||||    |||  :::
Db   4032 GTGGCTTCCCTTGGATCCAGCTTCAGGACACCCAAGAGCTG------------------ 4073

Qy     35 SerLeuValGlyLysSerHisGlnLysLysLeuProLeuAlaProSerMetGluAlaLeuGlu 54
                                ::::     |||||||       :::    ||||||
Db   4074 ---CTCCAAGAGAAACCCGGCAGAAGCTCAATGTGTCTACCAAGCTGCCTCAGTTGGAA 4130

Qy     54                                                                  54
Db   4131 GATGAAAGGAACAGCCTGCAGGACCAGCTGATGAGGAGGATGAGGGCTAAGCAAAACCTG 4190

Qy     55 ------------------LeuMetGlyValGlnPheValAspAlaLeuileLeuLysGlyGln 69
                              |||          |||  :::
Db   4191 GAGCGCCATGTCTCAACACTGAACATTCAGCTCTCCAGACTCTAAG---AAGAAGCTGCAG 4247

Qy     70 --------------------MetGluMetAlaLysGlyGlyGluAlaGluAspGlyAlaAspAsnGly 81
                               |||||||
Db   4248 GACTTTGCAAGTACCATCGAGTCTATGGAGGAGGGGAAGAAGAGGTTACAGAAAGAGATG 4307

Qy     82 GlyValLeuGluLysValHisProAspGln------------PheAspLysTyrLysLysLeu 98
            |||          :::   ||         ||
Db   4308 GAGGGGCCTCAGCCAGCAGTATGGAGGCGGCGGCTGCCTATGACAAACTGGAGAAAACC 4367

Qy     99 Lys------------------------ValAspAspLeuAlaAlaAspAlaValMetGlnIleAla 112
            |||                      :::
Db   4368 AAGAACAGGCTCCAGGAGAGCTGAGTCGTGGGACTTGGACAACCAGCGGCAA 4427

Qy    113 GluMetAlaLysLeuGlnProLysSerGlyAsnAlaPheIleAspMetLeuAsnGlyAsn 132
            ||||||     ||||||
Db   4428 CTGGTATCCAATCTGGAAAAGAGCAGGAAGAAA-----TTTGACCAGTTGTTAGCTGAG 4481

Qy    133 GlyIleProIleGlySerSer------------------------------------------- 139
            |||  |||
Db   4482 GAGAAGAACATCTCCTCCAAGTAGTCGGATGGCGATGAGAGACCAGGCTGAAGCAGAGGCCAGG 4541

Qy    140 ----------------------IleArgGlyLeuGluAspAlaIleArgThrGln 150
                                  ||    ||||
Db   4542 GAAAAGGAGACAAAGGCTTTGTCTCTAGCCCGGCCCTGGAAGCCCTGGAAGCCAAA 4601

Qy    151 ArgAspMetGluAsnThrAspProSerGluGlnIleAlaLysAlaValMetAspLysPhe 170
            ::::::        ||||
Db   4602 GAAGAGCTGGAGAGGAGGACCAAC-----------AAGATGCTCAAAGCTGAGATGAA-- 4646

Qy    171 GlnThrGlnIleLeuProGlyLeuValAlaAsnMet---IleAlaGlyLysAsnProPhe 189
            |||   ||||:::::
Db   4647 -----------GACCTGGTCAGCTCCAAGGAGATGATGTAGGCAGAACGTGCAT 4688

Qy    190 LysMetProGlnGlnMetArg---------------------------------------LysAlaGlnAla 200
            |||  :::         |||
Db   4689 GAACTGGAGAAGTCCAAGCGTGCCTTGGAGACCCAGATGGAAGAGATGAAAACCCAGCTG 4748

Qy    201 AlaProSerSerValPheGlnAlaGlnLeuAlaLeuAlaMetLeuGlyLysAsnAla 220
                       ||||      :::
Db   4749 GAGGAGTTCGGAGGATGAGCATGCCAAGCTGCGCGGCTAGAGGTC 4805

Qy    221 ProValAlaGlyLeuValArgGlyGluGlnGlnArgMetMetAsnArgValAspGlnArg 240
            |||      :::       :::|||
Db   4806 AACATGCAGGCCCTCAAGGCCAGTTTGAACCGCATCCCAGGCTCGGCGGATGAACAGAT 4865

Qy    241 MetGln---GlnArgGluLeuGlnGluGlu---AspGluAspAspGlnLeuAspAsp 258
            |||   :::             :::       :::
Db   4866 GAGGAGAAGAGAGGCAGGCTACAGCGGCAGCTACACGCGGCAGCTGCACGAGTATGAGAACAGAGAACTGGAAGAT 4925
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(right column, rotated)

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Qy    415 AlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAlaProArgLys 434
            :::         |||
Db  11855 GCCGAGAGCCCGCCAGCGTATCGAGTGGAGGCCCAG---GGTCACACCACACCGCACAAG 11799

Qy    435 IleProThrArgProLysMetLeuProLeuLeu------------------------- 446
            :::||||:::|||
Db  11798 CTCACAAGGAGGAGGAGCAGAAGGTCTTCTCCGGGGTGCGTGCTGGTGCACTGCCATCAAG 11739

Qy    447 ------------------IleGlySerAspProLysVal 453
                              ||||    :::
Db  11738 GGAGTGGGTGAAGTCCCGTGCCACTGCGCGCCGAGAGATTGGC---------AAGCTC 11688

Qy    454 GlnGluGluIleArgArgHisProSer------------------------------- 462
            :::||||        :::||
Db  11687 GAAGCCGAGGTCGAGAAGCACCGGAAGGACCTGGCCGCGCCTCCATGAGCACGGAGTC 11628

Qy    463 --------ThrGluTrpLysIleAlaLysGluSerArgValLeuThr------------- 475
                    :::||||     |||
Db  11627 GATGATGTGTGGGTCTGCGCGGCGGAGTGG-----GCGTCCCAGCAGGTCGTGCTTCAG 11574

Qy    476 AsnLeuLysAsnAsnProSerLeuAlaLeuAlaLeuPheMetAspAspLysLeuGluAsnThr 495
            |||              :::||||:::
Db  11573 GAGCTGTCGAACTACGAGGAGCACGGACCAGTTCTTGGAGGAC------AACAAA 11523

Qy    496 LeuLysGlyArgGlnMetLeuThrAspGluProIleGlnLysGlyArgThrValLysThrIle 515
            :::||||:::     |||:::    |||    :::
Db  11522 GTCGAGAGCGTCGAGTGTCCAAGGAACAGCAGAGGCAGGCACGG---AAGACG---- 11469

Qy    516 ArgAlaLeuProArgLeuPheGlyLysPheGlyThrAlaLysAlaAlaGluMetIleAspAlaLys 535
            :::          |||
Db  11468 --------GGGCCACTGAGCGCCCCAGCTCAACCTTTCGCGG--------- 11436

Qy    536 ValPheGlnIleGluGluArgProIlePro-----------ProLeuPheGluPro 552
            :::                    ||||
Db  11435 ------GAGGAGCTACAGACCCACCCATTTCCGACGCTGAGGCGTGACGGAGGAACTC 11382

Qy    553 LysGlyArgHisThrArgLeuArgTrpProThrGlyAlaAsnGluLysGluIleProGly 571
            :::|||:::
Db  11381 AAGGCCCCGCCAGCAGGAGGTGAAGGCCCGGACAAGGCGCGGGAGGAGGTGGAAGGA 11325
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RESULT 15
US-08-875-435B-1
; Sequence 1, Application US/08875435B
; Patent No. 6593304
; GENERAL INFORMATION:
; APPLICANT: Hasegawa, Kazuhide
; APPLICANT: Arakawa, Emi
; APPLICANT: Oda, Shoji
; APPLICANT: Matsuda, Yuzuru
; APPLICANT: Takahashi, Katsuhito
; APPLICANT: Sugahara, Michihiro
; APPLICANT: Ishiyama, Haruo
; TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
; TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
; TITLE OF INVENTION: VECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, AND
; TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
; TITLE OF INVENTION: RECOMBINANT DNA
; FILE REFERENCE: 07898-013001
; CURRENT APPLICATION NUMBER: US/08/875,435B
; CURRENT FILING DATE: 1997-07-25
; PRIOR APPLICATION NUMBER: PCT/JP96/00134
; PRIOR FILING DATE: 1996-01-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6175
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (105)...(6020)
US-08-875-435B-1
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Mon Mar  6 09:44:50 2006

us-10-736-868-2.p2n.rni

Search completed: March  3, 2006, 18:41:26
Job time : 462 secs

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Qy   259 GluAspValProArgArgSerSerAspGlyGluProGlnSerGlyAlaGluHisGln 278
             :::::|||||||::::        :::  |||
Db  4926 GAA------CGGAAGCAGAGCTCTGGCGCGCAGCTAAGAAGAAGCTGAAGGGGAC 4979

Qy   279 ArgArgAspLeuAlaAlaArgArgLeuLysSerProArgLeuLysGlu-----LeuLeu 296
             :::|||||||          :::  |||
Db  4980 CTAAAAGACCTAGAGCTCCAGGCTGACTCAGCCATCAAAGGGAGGAGAAGCCATCAAG 5039

Qy   297 GlnAsnAlaGluValGlnSer---LeuLeuSerTyrGlnArg---MetArgAspSerPro 314
             |||::::|||::::  :::|||||        :::  |||
Db  5040 CAGCTTCGAAAACTGCGAGGCTCAGATGAAGGACTTCCAAAGAGAGCTGGATGATGCCCGT 5099

Qy   315 LeuSerLysArgArgProLeuAlaMetAsnAspGluAspSerAlaPheArgAlaMet 334
             |||::::        |||  :::::::::|||::::||
Db  5100 GCCTCCAGGGATGAGATCTTTGCCACCTCAAAAGAATGAGAAGAAAGCCAAGAGTCTG 5159

Qy   335 GluAla------------------------------------------------Arg 337
             |||||                                              :::
Db  5160 GAGGCAGGAGACCTCATGCAGCTCCCAAGAGGACCTGGCAGCTGAGAGCTCGCAAGCAA 5219

Qy   338 AlaLysLeuAspGlnLys-------SerGlnLeuValLeuGlyLeuHisGlyPheGly 354
             |||||::::::::          :::|||
Db  5220 GCTGACCTGGAAGAAGGAGAGAGGCTGGCCGAGAGCTTGGCTAGCAGCTTGTCAGGAGGAAT 5279

Qy   355 GluSerAspAsp-----------------------------------AspGluAsp 361
             |||:::                                          |||
Db  5280 ACACTGCAGGATGAGATGAGGAAGCGCCGCCTGGAGGCAAGGATCGCCCAACTAGGAGGAGCTG 5339

Qy   362 GluGluAspGluAsnLeuIleAspProSerGluGlnSerPheArgArgAlaProLeu--- 380
             |||::::  :::        ||      :::::::|||
Db  5340 GAGGAAGAGGACGAGGGCCAACATGGAGGCCATGAGTGATAGATAGTACGCAAGGCCACACTGCAG 5399

Qy   381 ------ArgLeuSerSerGlyPheValGluLys--------LeuLysSerAsnAspGlu 395
             :::|||||||        :::  |||::::||
Db  5400 GCTGAGCAACTGGCAATGAGCTGCCACAGAACGCACGGCTCAGAGAAGAATGAGAGC 5459

Qy   396 LeuLysSerAlaLeuAspArg------------IleLysTyrArgValAspAspValGlu 411
             :::|||||||                    :::::::  ::::||||||
Db  5460 GCACGGCAACCTGGAGCCGGCAGCGCCAGACAACAAGGAACGTTGCGAGGCAGGTAGAA 5519

Qy   412 LysTyrLeuAlaProLysProMetGluPheAsnProLysProGlnProGlyTyrPheAla 431
Db  5519 ----------------------------------------------------------- 5519

Qy   432 ProArgLysIleProThrArgProArgLysMetLeuProLeuLeuIleGlySerAspPro 451
             :::                        :::
Db  5520 --GGTGCTGTCAAAGCCAAGCTCAAGTCCACTGTTGCGGCGCCTGGAGGCCAAGATTGCA 5576

Qy   452 LysValGlnGluGluLeuArgArgHisProSerThrArgValLysThrArgLeuLysGluSer 471
             :::::::::::||||||  :::::::::||
Db  5577 CAGCTGGAGGCAGGTTGAACAGGAG------------------GCCAGAGAAA 5615

Qy   472 ArgValLeuThr---AsnLeuLysAsnAsnProSerLeuAlaAlaLeuPheMetCysAspAsp 490
             :::        |||:::||                              -----GACAAG
Db  5616 CAGGCCGCCACCAAGTCGCTGAAGCAAAAG-----------------------GACAAG 5651

Qy   491 LysLeuGluAsnThrLeu--------------------------LysGlyLysArgGlnMetLeu 502
             :::|||::::                                  ||
Db  5652 AAGCTAAAGGAGGTTCCTGCTGCAGGTGAAGGATGAGGCGCAAGAGCAGTACAAG 5711

Qy   503 ThrAspGluGlnLysGlyArgThrArgValLysThrArgIleAlaLeuProArgLeuPhe 522
             :::::::||::::||||||  :::::::
Db  5712 GAGCAGGCCAGGCAGGAAAGGAAACACCCAAGGTCAAGACCTGAAG------AGGCAGCTG 5762

Qy   523 GlyAlaProThrAlaLysAlaGluMetIleAspAla-------LysValPheGlnAsp 539
             |||:::        |||||::::||  :::::::||
Db  5763 GAAGAGGCCGAGGAGGAGTCCCAGTGCATCAACGCCAACCCCAGGAAGCTCCAGCGCGGGAG 5822

Qy   540 IleGluGlu 542
             :::::|||
Db  5823 CTAGATGAG 5831
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